

FIG.1A

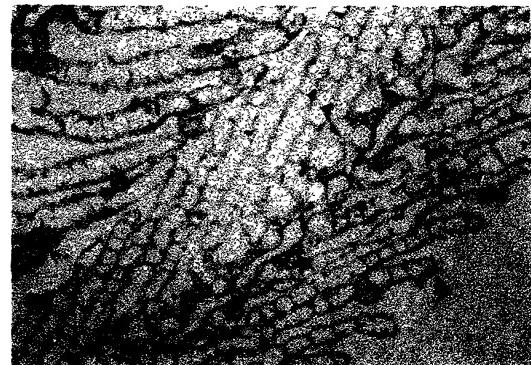


FIG.1B

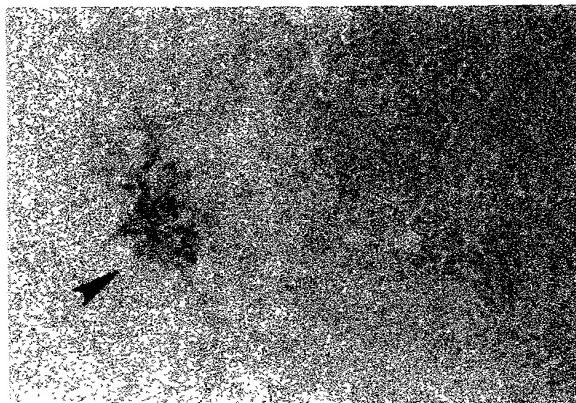


FIG.1C

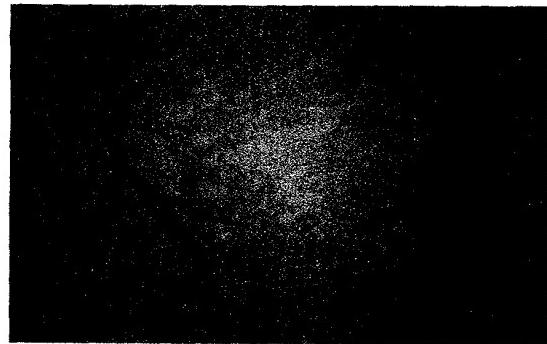


FIG.1D

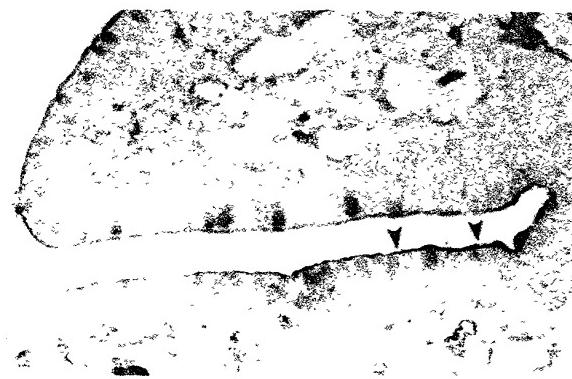


FIG.1E

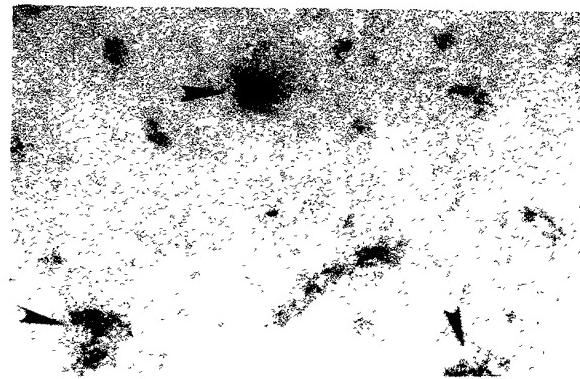


FIG.1F

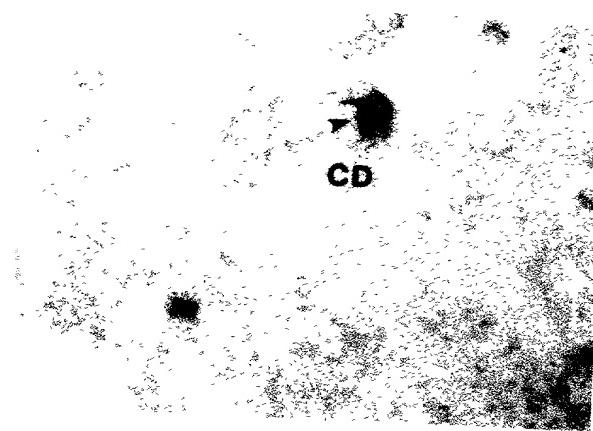


FIG.2A

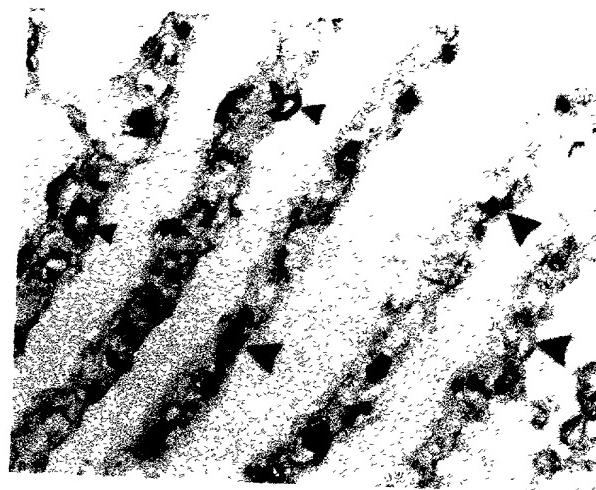


FIG.2B

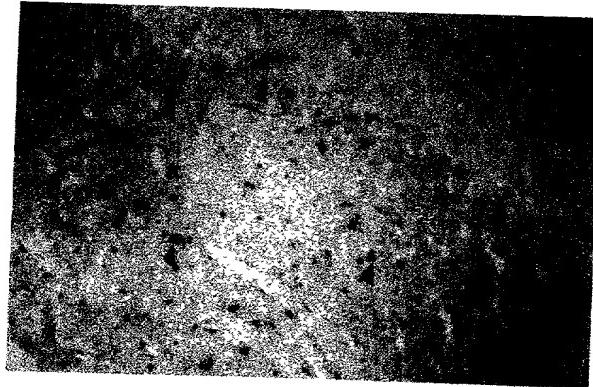


FIG.2C

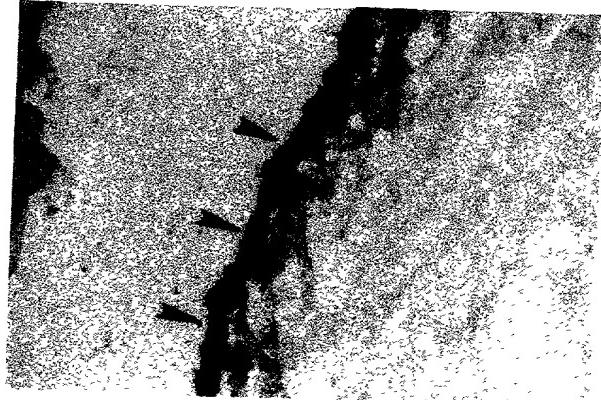


FIG.2D

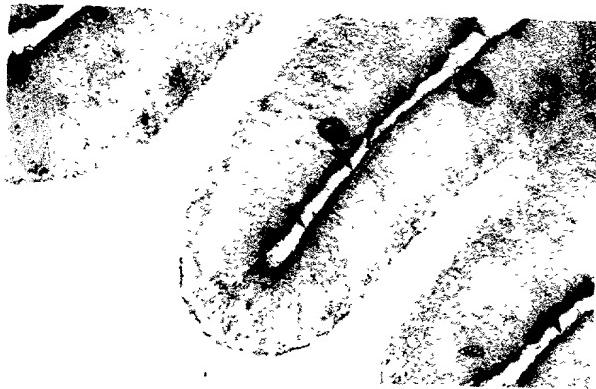


FIG.2E

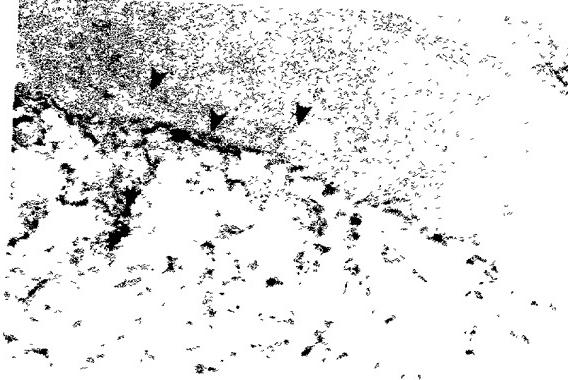


FIG.2F

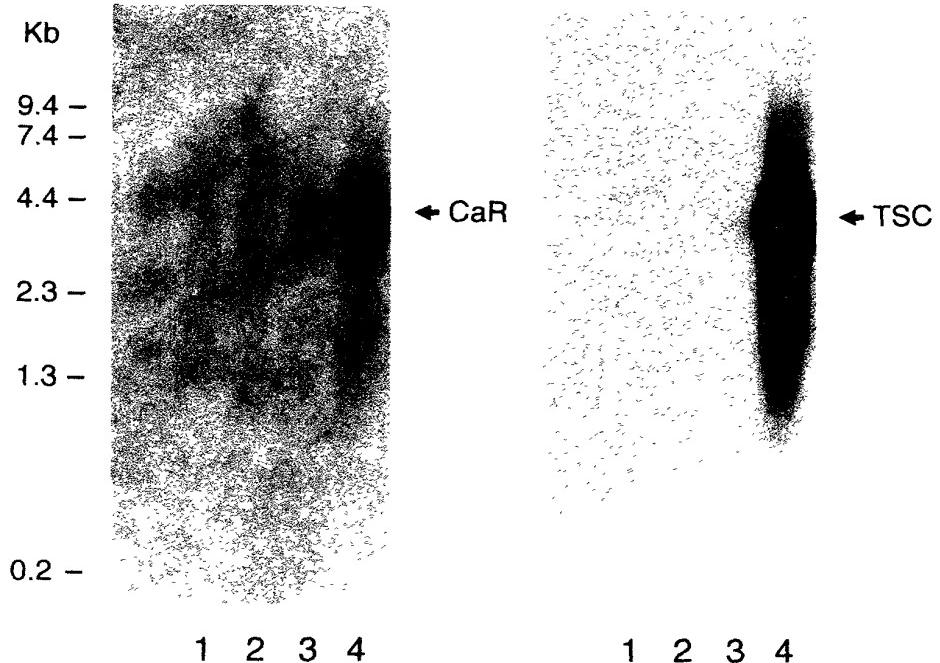


FIG.3A

FIG.3B

aattccgttg ctgtcggttc agtccaagtc tcctccagtg caaaatgaga aatgggtggc 60		
gccattacag gaacatgcac tacatctgt ttaatgaat attgtcagtt atctgaagg 120		
tataaaaatg ttctgcaag gatggctca cgagaaatca attctgcacg ttttcccatt 180		
gtcattgtat gaataactga ccaaaggat gtaacaaaat ggaacaaagc tgaggaccac 240		
gttcaccctt tcttgagca tacgatcaac cctgaaggag atggaagact tgaggaggaa 300		
atggggattg atcttccagg agttctgctg taaagcgatc cctcaccatt acaaagataa 360		
gcagaaaatcc tccaggcattc ctctgtaaac gggctggcgt agtgtggcgtt ggtcaaggaa 420		
cagagacagg gctgcaca atg gct ctt cac tgc caa ctc tta ttc ttg 471		
Met Ala Gln Leu His Cys Gln Leu Leu Phe Leu		
1 5 10		
gga ttt aca ctc cta cag tcg tac aat gtc tca ggg tat ggt cca aac 519		
Gly Phe Thr Leu Leu Gln Ser Tyr Asn Val Ser Gly Tyr Gly Pro Asn		
15 20 25		
caa agg gcc cag aag aaa gga gac atc ata ctg gga ggt ctc ttc cca 567		
Gln Arg Ala Gln Lys Lys Gly Asp Ile Ile Leu Gly Gly Leu Phe Pro		
30 35 40		
ata cac ttt gga gta gcc gcc aag gat cag gac tta aaa tcg aga ccg 615		
Ile His Phe Gly Val Ala Ala Lys Asp Gln Asp Leu Lys Ser Arg Pro		
45 50 55		
gag gcg aca aaa tgt att cgg tac aat ttt cga ggc ttc cga tgg ctc 663		
Glu Ala Thr Lys Cys Ile Arg Tyr Asn Phe Arg Gly Phe Arg Trp Leu		
60 65 70 75		
cag gcg atg ata ttc gca att gaa gag att aac aac agt atg act ttc 711		
Gln Ala Met Ile Phe Ala Ile Glu Glu Ile Asn Asn Ser Met Thr Phe		
80 85 90		
ctg ccc aat atc acc ctg gga tat cgc ata ttt gac acg tgt aac acc 759		
Leu Pro Asn Ile Thr Leu Gly Tyr Arg Ile Phe Asp Thr Cys Asn Thr		
95 100 105		
gtg tcc aag gcg cta gag gca aca ctc agc ttt gtg gcc cag aac aaa 807		
Val Ser Lys Ala Leu Glu Ala Thr Leu Ser Phe Val Ala Gln Asn Lys		
110 115 120		
atc gac tcg ctg aac tta gat gag ttc tgt aac tgc tct gac cat atc 855		
Ile Asp Ser Leu Asn Leu Asp Glu Phe Cys Asn Cys Ser Asp His Ile		
125 130 135		
cca tcc aca ata gca gtg gtc ggg gca acc ggg tca gga atc tcc acg 903		
Pro Ser Thr Ile Ala Val Val Gly Ala Thr Gly Ser Gly Ile Ser Thr		
140 145 150 155		
gct gtg gcc aat cta ttg gga tta ttt tac att cca cag gtc agc tat 951		
Ala Val Ala Asn Leu Leu Gly Leu Phe Tyr Ile Pro Gln Val Ser Tyr		
160 165 170		
gcc tcc tcg agc agg ctg ctc agc aac aag aat gag tac aag gcc ttc 999		
Ala Ser Ser Arg Leu Leu Ser Asn Lys Asn Glu Tyr Lys Ala Phe		
175 180 185		
ctg agg acc atc ccc aat gat gag caa cag gcc acg gcc atg gcc gag 1047		
Leu Arg Thr Ile Pro Asn Asp Glu Gln Gln Ala Thr Ala Met Ala Glu		
190 195 200		

FIG. 4A

atc atc gag cac ttc cag tgg aac tgg gtg gga acc ctg gca gcc gac Ile Ile Glu His Phe Gln Trp Asn Trp Val Gly Thr Leu Ala Ala Asp 205 210 215	1095
gat gac tat ggc cgc cca ggc att gac aag ttc cgg gag gag gcc gtt Asp Asp Tyr Gly Arg Pro Gly Ile Asp Lys Phe Arg Glu Glu Ala Val 220 225 230 235	1143
aag agg gag atc tgt att gac ttc agt gag atg atc tct cag tac tac Lys Arg Asp Ile Cys Ile Asp Phe Ser Glu Met Ile Ser Gln Tyr Tyr 240 245 250	1191
acc cag aag cag ttg gag ttc atc gcc gac gtc atc cag aac tcc tcg Thr Gln Lys Gln Leu Glu Phe Ile Ala Asp Val Ile Gln Asn Ser Ser 255 260 265	1239
gcc aag gtc atc gtg gtc ttc tcc aat ggc ccc gac ctg gag ccg ctc Ala Lys Val Ile Val Val Phe Ser Asn Gly Pro Asp Leu Glu Pro Leu 270 275 280	1287
atc cag gag ata gtt cgg aga aac atc acc gat cgg atc tgg ctg gcc Ile Gln Glu Ile Val Arg Arg Asn Ile Thr Asp Arg Ile Trp Leu Ala 285 290 295	1335
agc gag gct tgg gcc agc tct tcg ctc att gcc aag cca gag tac ttc Ser Glu Ala Trp Ala Ser Ser Leu Ile Ala Lys Pro Glu Tyr Phe 300 305 310 315	1383
cac gtg gtc ggc ggc acc atc ggc ttc gct ctc agg gcg ggg cgt atc His Val Val Gly Gly Thr Ile Gly Phe Ala Leu Arg Ala Gly Arg Ile 320 325 330	1431
cca ggg ttc aac aag ttc ctg aag gag gtc cac ccc agc agg tcc tcg Pro Gly Phe Asn Lys Phe Leu Lys Glu Val His Pro Ser Arg Ser Ser 335 340 345	1479
gac aat ggg ttt gtc aag gag ttc tgg gag gag acc ttc aac tgc tac Asp Asn Gly Phe Val Lys Glu Phe Trp Glu Glu Thr Phe Asn Cys Tyr 350 355 360	1527
ttc acc gag aag acc ctg acg cag ctg aag aat tcc aag gtg ccc tcg Phe Thr Glu Lys Thr Leu Thr Gln Leu Lys Asn Ser Lys Val Pro Ser 365 370 375	1575
cac gga ccg gcg gct caa ggg gac ggc tcc aag gcg ggg aac tcc aga His Gly Pro Ala Ala Gln Gly Asp Gly Ser Lys Ala Gly Asn Ser Arg 380 385 390 395	1623
cgg aca gcc cta cgc cac ccc tgc act ggg gag gag aac atc acc agc Arg Thr Ala Leu Arg His Pro Cys Thr Gly Glu Glu Asn Ile Thr Ser 400 405 410	1671
gtg gag acc ccc tac ctg gat tat aca cac ctg agg atc tcc tac aat Val Glu Thr Pro Tyr Leu Asp Tyr Thr His Leu Arg Ile Ser Tyr Asn 415 420 425	1719
gta tac gtg gcc gtc tac tcc att gct cac gcc ctg caa gac atc cac Val Tyr Val Ala Val Tyr Ser Ile Ala His Ala Leu Gln Asp Ile His 430 435 440	1767

tct tgc aaa ccc ggc acg-ggc atc ttt gca aac gga tct tgt gca gat Ser Cys Lys Pro Gly Thr Gly Ile Phe Ala Asn Gly Ser Cys Ala Asp 445 450 455	1815
att aaa aaa gtt gag gcc tgg cag gtc ctc aac cat ctg ctg cat ctg Ile Lys Lys Val Glu Ala Trp Gln Val Leu Asn His Leu Leu His Leu 460 465 470 475	1863
aag ttt acc aac agc atg ggt gag cag gtt gac ttt gac gat caa ggt Lys Phe Thr Asn Ser Met Gly Glu Gln Val Asp Phe Asp Asp Gln Gly 480 485 490	1911
gac ctc aag ggg aac tac acc att atc aac tgg cag ctc tcc gca gag Asp Leu Lys Gly Asn Tyr Thr Ile Ile Asn Trp Gln Leu Ser Ala Glu 495 500 505	1959
gat gaa tcg gtg ttg ttc cat gag gtg ggc aac tac aac gcc tac gct Asp Glu Ser Val Leu Phe His Glu Val Gly Asn Tyr Asn Ala Tyr Ala 510 515 520	2007
aag ccc agt gac cga ctc aac atc aac gaa aag aaa atc ctc tgg agt Lys Pro Ser Asp Arg Leu Asn Ile Asn Glu Lys Lys Ile Leu Trp Ser 525 530 535	2055
ggc ttc tcc aaa gtg gtt cct ttc tcc aac tgc agt cga gac tgt gtg Gly Phe Ser Lys Val Val Pro Phe Ser Asn Cys Ser Arg Asp Cys Val 540 545 550 555	2103
ccg ggc acc agg aag ggg atc atc gag ggg gag ccc acc tgc tgc ttt Pro Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr Cys Cys Phe 560 565 570	2151
gaa tgc atg gca tgt gca gag gga gag ttc agt gat gaa aac gat gca Glu Cys Met Ala Cys Ala Glu Gly Glu Phe Ser Asp Glu Asn Asp Ala 575 580 585	2199
agt gcg tgt aca aag tgc ccg aat gat ttc tgg tcg aat gag aac cac Ser Ala Cys Thr Lys Cys Pro Asn Asp Phe Trp Ser Asn Glu Asn His 590 595 600	2247
acg tcg tgc atc gcc aag gag atc gag tac ctg tcg tgg acg gag ccc Thr Ser Cys Ile Ala Lys Glu Ile Glu Tyr Leu Ser Trp Thr Glu Pro 605 610 615	2295
ttc ggg atc gct ctg acc atc ttc gcc gta ctg ggc atc ctg atc acc Phe Gly Ile Ala Leu Thr Ile Phe Ala Val Leu Gly Ile Leu Ile Thr 620 625 630 635	2343
tcc ttc gtg ctg ggg gtc ttc atc aag ttc agg aac act ccc atc gtg Ser Phe Val Leu Gly Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val 640 645 650	2391
aag gcc acc aac cgg gag ttg tcc tac ctg ctg ctc ttc tcc ctc atc Lys Ala Thr Asn Arg Glu Leu Ser Tyr Leu Leu Leu Phe Ser Leu Ile 655 660 665	2439
tgc tgc ttc tcc agc tcg ctc atc ttc atc ggc gag ccc agg gac tgg Cys Cys Phe Ser Ser Ser Leu Ile Phe Ile Gly Glu Pro Arg Asp Trp 670 675 680	2487

acc tgt cgg ctc cgc caa-ccg gcc ttt ggc atc agc ttc gtc ctg tgc	2535
Thr Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys	
685 690 695	
atc tcc tgc atc ctg gtg aag acc aac cgg gtg ctg ctg gtc ttc gag	2583
Ile Ser Cys Ile Leu Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu	
700 705 710 715	
gcc aag atc ccc acc agc ctc cac cgc aag tgg gtg ggc ctc aac ctg	2631
Ala Lys Ile Pro Thr Ser Leu His Arg Lys Trp Val Gly Leu Asn Leu	
720 725 730	
cag ttc ctc ctg gtc ttc ctc tgc atc ctg gtg caa atc gtc acc tgc	2679
Gln Phe Leu Leu Val Phe Leu Cys Ile Leu Val Gln Ile Val Thr Cys	
735 740 745	
atc atc tgg ctc tac acc gcg cct ccc tcc agc tac agg aac cat gag	2727
Ile Ile Trp Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg Asn His Glu	
750 755 760	
ctg gag gac gag gtc atc ttc atc acc tgc gac gag ggc tcg ctc atg	2775
Leu Glu Asp Glu Val Ile Phe Ile Thr Cys Asp Glu Gly Ser Leu Met	
765 770 775	
gcg ctg ggc ttc ctc atc ggc tac acc tgc ctc ctc gcc gcc atc tgc	2823
Ala Leu Gly Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys	
780 785 790 795	
ttc ttc ttc gcc ttc aag tcc cgt aag ctg ccg gag aac ttc aac gag	2871
Phe Phe Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn Glu	
800 805 810	
gct aag ttc atc acc ttc agc atg ttg atc ttc ttc atc gtc tgg atc	2919
Ala Lys Phe Ile Thr Phe Ser Met Leu Ile Phe Phe Ile Val Trp Ile	
815 820 825	
tcc ttc atc ccc gcc tat gtc agc acc tac ggc aag ttt gtg tcg gcc	2967
Ser Phe Ile Pro Ala Tyr Val Ser Thr Tyr Gly Lys Phe Val Ser Ala	
830 835 840	
gtg gag gtg att gcc atc ctg gcc tcc agc ttc ggg ctg ctg ggc tgc	3015
Val Glu Val Ile Ala Ile Leu Ala Ser Ser Phe Gly Leu Leu Gly Cys	
845 850 855	
att tac ttc aac aag tgt tac atc atc ctg ttc aag ccg tgc cgt aac	3063
Ile Tyr Phe Asn Lys Cys Tyr Ile Ile Leu Phe Lys Pro Cys Arg Asn	
860 865 870 875	
acc atc gag gag gtg cgc tgc agc acg gcg gcc cac gcc ttc aag gtg	3111
Thr Ile Glu Glu Val Arg Cys Ser Thr Ala Ala His Ala Phe Lys Val	
880 885 890	
gcg gcc cgg gcc acc ctc cgg cgc agc gcc gcg tct cgc aag cgc tcc	3159
Ala Ala Arg Ala Thr Leu Arg Arg Ser Ala Ala Ser Arg Lys Arg Ser	
895 900 905	
agc agc ctg tgc ggc tcc acc atc tcc tcg ccc gcc tcg tcc acc tgc	3207
Ser Ser Leu Cys Gly Ser Thr Ile Ser Ser Pro Ala Ser Ser Thr Cys	
910 915 920	

ggg ccg ggc ctc acc atg-gag atg cag cgc tgc agc acg cag aag gtc 3255
Gly Pro Gly Leu Thr Met Glu Met Gln Arg Cys Ser Thr Gln Lys Val
925 930 935

agc ttc ggc agc ggc acc gtc acc ctg tcg ctc agc ttc gag gag aca 3303
Ser Phe Gly Ser Gly Thr Val Thr Leu Ser Leu Ser Phe Glu Glu Thr
940 945 950 955

ggc cga tac gcc acc ctc agc cgc acg gcc cgc agc agg aac tcg gcg 3351
Gly Arg Tyr Ala Thr Leu Ser Arg Thr Ala Arg Ser Arg Asn Ser Ala
960 965 970

gat ggc cgc agc ggc gac gac ctg cca tct aga cac cac gac cag ggc 3399
Asp Gly Arg Ser Gly Asp Asp Leu Pro Ser Arg His His Asp Gln Gly
975 980 985

ccg cct cag aaa tgc gag ccc cag ccc gcc aac gat gcc cga tac aag 3447
Pro Pro Gln Lys Cys Glu Pro Gln Pro Ala Asn Asp Ala Arg Tyr Lys
990 995 1000

gcg gcg ccg acc aag ggc acc cta gag tcg ccg ggc ggc agc aag gag 3495
Ala Ala Pro Thr Lys Gly Thr Leu Glu Ser Pro Gly Gly Ser Lys Glu
1005 1010 1015

cgc ccc aca act atg gag gaa acc taa tccaaactcct ccatcaaccc 3542
Arg Pro Thr Thr Met Glu Glu Thr *
1020 1025

caagaacatc ctccacggca gcaccgtcga caactgacat caactcctaa ccgggtggctg 3602
cccaacctct cccctctccg gcactttgcg ttttgcgtaa gattgcagca tctgcagtcc 3662
cttttatccc tgatttctg acttgatata ttacttagtgt gcgtatggaat atcacaaacat 3722
aatgagttgc acaatttaggt gagcagagtt gtgtcaaagt atctgaacta tctgaaggat 3782
ctgaactact ttattctctc gaattgttatt acaaacattt gaagtatttt tagtgacatt 3842
atgttctaaac attgtcaaga taatttgttta caacatataa ggtaccacct gaagcagtga 3902
ctgagatgtc cactgtgtatc acagaactgt tttataacat ttatcattga aacctggatt 3962
gcaacagaaa tataatgact gtaaaaaaaa aattgttgat tatctaaaaa atgcaaattg 4022
taatcagatg tgtaaaaattg gtaattactt ctgtacatata aatgcatatt tcttgataaa 4082
aaaaaaaaaaaa aaaaaaaaaaaa aaaagcggcc cgacagcaac gg 4134

FIG. 4E

aattccgttg ctgtcggttc agtccaagtc tcctccagtg caaaaatgaga aatgggtggtc 60
 gccattacag gaacatgcac tacatctgt ttaatgaaat attgtcagg atctgaaggt 120
 tattaaaatg tttctgcaag gatggcttca cgagaaaatca attctgcacg ttttcccatt 180
 gtcattgtat gaataactga ccaaaggat gtaacaaaat ggaacaaaagc tgaggaccac 240
 gttcacccctt tcctggagca tacatcaac cctgaaggag atggaagact tgaggaggaa 300
 atggggattg atcttccagg agttctgctg taaagcgatc cctcaccatt acaaagataa 360
 gcagaaaatcc tccaggcatc ctctgtaaac gggctggcgt agtgtggcctt ggtcaaggaa 420
 cagagacagg gctgcaca atg gct cag ctt cac tgc caa ctc tta ttc ttg 471
 Met Ala Gln Leu His Cys Gln Leu Leu Phe Leu
 1 5 10

gga ttt aca ctc cta cag tcg tac aat gtc tca ggg tat ggt cca aac 519
 Gly Phe Thr Leu Leu Gln Ser Tyr Asn Val Ser Gly Tyr Gly Pro Asn
 15 20 25

caa agg gcc cag aag aaa gga gac atc ata ctg gga ggt ctc ttc cca 567
 Gln Arg Ala Gln Lys Lys Gly Asp Ile Ile Leu Gly Gly Leu Phe Pro
 30 35 40

ata cac ttt gga gta gcc gcc aag gat cag gac tta aaa tcg aga ccg 615
 Ile His Phe Gly Val Ala Ala Lys Asp Gln Asp Leu Lys Ser Arg Pro
 45 50 55

gag gcg aca aaa tgt att cgg tac aat ttt cga ggc ttc cga tgg ctc 663
 Glu Ala Thr Lys Cys Ile Arg Tyr Asn Phe Arg Gly Phe Arg Trp Leu
 60 65 70 75

cag gcg atg ata ttc gca att gaa gag att aac aac agt atg act ttc 711
 Gln Ala Met Ile Phe Ala Ile Glu Glu Ile Asn Asn Ser Met Thr Phe
 80 85 90

ctg ccc aat atc acc ctg gga tat cgc ata ttt gac acg tgt aac acc 759
 Leu Pro Asn Ile Thr Leu Gly Tyr Arg Ile Phe Asp Thr Cys Asn Thr
 95 100 105

gtg tcc aag gcg cta gag gca aca ctc agc ttt gtg gcc cag aac aaa 807
 Val Ser Lys Ala Leu Glu Ala Thr Leu Ser Phe Val Ala Gln Asn Lys
 110 115 120

atc gac tcg ctg aac tta gat gag ttc tgt aac tgc tct gac cat atc 855
 Ile Asp Ser Leu Asn Leu Asp Glu Phe Cys Asn Cys Ser Asp His Ile
 125 130 135

cca tcc aca ata gca gtg gtc ggg gca acc ggg tca gga atc tcc acg 903
 Pro Ser Thr Ile Ala Val Val Gly Ala Thr Gly Ser Gly Ile Ser Thr
 140 145 150 155

gct gtg gcc aat cta ttg gga tta ttt tac att cca cag gtc agc tat 951
 Ala Val Ala Asn Leu Leu Gly Leu Phe Tyr Ile Pro Gln Val Ser Tyr
 160 165 170

gcc tcc tcg agc agg ctg ctc agc aac aag aat gag tac aag gcc ttc 999
 Ala Ser Ser Arg Leu Leu Ser Asn Lys Asn Glu Tyr Lys Ala Phe
 175 180 185

ctg agg acc atc ccc aat gat gag caa cag gcc acg gcc atg gcc gag 1047
 Leu Arg Thr Ile Pro Asn Asp Glu Gln Gln Ala Thr Ala Met Ala Glu
 190 195 200

100-16436-1001-0001

atc atc gag cac ttc cag tgg aac tgg gtg gga acc ctg gca gcc gac 1095
Ile Ile Glu His Phe Gln Trp Asn Trp Val Gly Thr Leu Ala Ala Asp
205 210 215

gat gac tat ggc cgc cca ggc att gac aag ttc cgg gag gag gcc gtt 1143
Asp Asp Tyr Gly Arg Pro Gly Ile Asp Lys Phe Arg Glu Glu Ala Val
220 225 230 235

aag agg gag atc tgt att gac ttc agt gag atg atc tct cag tac tac 1191
Lys Arg Asp Ile Cys Ile Asp Phe Ser Glu Met Ile Ser Gln Tyr Tyr
240 245 250

acc cag aag cag ttg gag ttc atc gcc gac gtc atc cag aac tcc tcg 1239
Thr Gln Lys Gln Leu Glu Phe Ile Ala Asp Val Ile Gln Asn Ser Ser
255 260 265

gcc aag gtc atc gtg gtc ttc tcc aat ggc ccc gac ctg gag ccg ctc 1287
Ala Lys Val Ile Val Val Phe Ser Asn Gly Pro Asp Leu Glu Pro Leu
270 275 280

atc cag gag ata gtt cgg aga aac atc acc gat cgg atc tgg ctg gcc 1335
Ile Gln Glu Ile Val Arg Arg Asn Ile Thr Asp Arg Ile Trp Leu Ala
285 290 295

agc gag gct tgg gcc agc tct tcg ctc att gcc aag cca gag tac ttc 1383
Ser Glu Ala Trp Ala Ser Ser Leu Ile Ala Lys Pro Glu Tyr Phe
300 305 310 315

cac gtg gtc ggc ggc acc atc ggc ttc gct ctc agg gcg ggg cgt atc 1431
His Val Val Gly Gly Thr Ile Gly Phe Ala Leu Arg Ala Gly Arg Ile
320 325 330

cca ggg ttc aac aag ttc ctg aag gag gtc cac ccc agc agg tcc tcg 1479
Pro Gly Phe Asn Lys Phe Leu Lys Glu Val His Pro Ser Arg Ser Ser
335 340 345

gac aat ggg ttt gtc aag gag ttc tgg gag gag acc ttc aac tgc tac 1527
Asp Asn Gly Phe Val Lys Glu Phe Trp Glu Glu Thr Phe Asn Cys Tyr
350 355 360

tcc acc gag aag acc ctg acg cag ctg aag aat tcc aag gtg ccc tcg 1575
Phe Thr Glu Lys Thr Leu Thr Gln Leu Lys Asn Ser Lys Val Pro Ser
365 370 375

cac gga ccg gcg gct caa ggg gac ggc tcc aag gcg ggg aac tcc aga 1623
His Gly Pro Ala Ala Gln Gly Asp Gly Ser Lys Ala Gly Asn Ser Arg
380 385 390 395

cgg aca gcc cta cgc cac ccc tgc act ggg gag gag aac atc acc agc 1671
Arg Thr Ala Leu Arg His Pro Cys Thr Gly Glu Glu Asn Ile Thr Ser
400 405 410

gtg gag acc ccc tac ctg gat tat aca cac ctg agg atc tcc tac aat 1719
Val Glu Thr Pro Tyr Leu Asp Tyr Thr His Leu Arg Ile Ser Tyr Asn
415 420 425

gta tac gtg gcc gtc tac tcc att gct cac gcc ctg caa gac atc cac 1767
Val Tyr Val Ala Val Tyr Ser Ile Ala His Ala Leu Gln Asp Ile His
430 435 440

tct tgc aaa ccc ggc acg	ggc atc ttt gca aac	gga tct tgt gca gat	1815
Ser Cys Lys Pro Gly Thr	Gly Ile Phe Ala Asn	Gly Ser Cys Ala Asp	
445	450	455	
att aaa aaa gtt gag gcc	tgg cag gtc ctc aac	cat ctg ctg cat ctg	1863
Ile Lys Lys Val Glu Ala	Trp Gln Val Leu Asn	His Leu Leu His Leu	
460	465	470	475
aag ttt acc aac agc atg	ggt gag cag gtt gac	ttt gac gat caa ggt	1911
Lys Phe Thr Asn Ser Met	Gly Gln Val Asp Phe	Asp Asp Gln Gly	
480	485	490	
gac ctc aag ggg aac tac	acc att atc aac tgg cag	ctc tcc gca gag	1959
Asp Leu Lys Gly Asn Tyr	Thr Ile Ile Asn Trp Gln	Leu Ser Ala Glu	
495	500	505	
gat gaa tcg gtg ttg ttc	cat gag gtg ggc aac	tac aac gcc tac gct	2007
Asp Glu Ser Val Leu Phe	His Glu Val Gly Asn	Tyr Asn Ala Tyr Ala	
510	515	520	
aag ccc agt gac cga ctc	aac atc aac gaa aag	aaa atc ctc tgg agt	2055
Lys Pro Ser Asp Arg Leu	Asn Ile Asn Glu Lys	Ile Leu Trp Ser	
525	530	535	
ggc ttc tcc aaa gtg gtt	cct ttc tcc aac tgc agt	cga gac tgt gtg	2103
Gly Phe Ser Lys Val Val	Pro Phe Ser Asn Cys	Ser Arg Asp Cys Val	
540	545	550	555
ccg ggc acc agg aag ggg	atc atc gag ggg gag	ccc acc tgc tgc ttt	2151
Pro Gly Thr Arg Lys Gly	Ile Ile Glu Gly Pro	Thr Cys Cys Phe	
560	565	570	
gaa tgc atg gca tgt	gca gag gga gag	ttc agt gat gaa aac	2199
Glu Cys Met Ala Cys Ala	Glu Phe Ser Asp Glu	Asn Asp Ala	
575	580	585	
agt gcg tgt aca aag tgc	ccg aat gat ttc tgg	tgc aat gag aac cac	2247
Ser Ala Cys Thr Lys Cys	Pro Asn Asp Phe Trp	Ser Asn Glu Asn His	
590	595	600	
acg tcg tgc atc gcc aag	gag atc gag tac ctg	tgc tgg acg gag ccc	2295
Thr Ser Cys Ile Ala Lys	Glu Ile Glu Tyr Leu	Ser Trp Thr Glu Pro	
605	610	615	
ttc ggg atc gct ctg acc	atc ttc gcc gta	ctg ggc atc ctg atc acc	2343
Phe Gly Ile Ala Leu Thr	Ile Phe Ala Val	Leu Gly Ile Leu Ile Thr	
620	625	630	635
tcc ttc gtg ctg ggg gtc	ttc atc aag ttc	agg aac act ccc atc gtg	2391
Ser Phe Val Leu Gly Val	Phe Ile Lys Phe Arg	Asn Thr Pro Ile Val	
640	645	650	
aag gcc acc aac cgg gag	ttg tcc tac ctg	ctg ctc ttc tcc ctc atc	2439
Lys Ala Thr Asn Arg Glu	Leu Ser Tyr Leu	Leu Phe Ser Leu Ile	
655	660	665	
tgc tgc ttc tcc agc	tcg ctc atc ttc	atc ggc gag ccc agg gac tgg	2487
Cys Cys Phe Ser Ser	Leu Ile Phe Ile	Gly Glu Pro Arg Asp Trp	
670	675	680	

acc tgt cgg ctc cgc caa ccg gcc ttt ggc atc agc ttc gtc ctg tgc 2535
Thr Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys
685 690 695

atc tcc tgc atc ctg gtg aag acc aac cgg gtg ctg ctg gtc ttc gag 2583
Ile Ser Cys Ile Leu Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu
700 705 710 715

gcc aag atc ccc acc agc ctc cac cgc aag tgg gtg ggc ctc aac ctg 2631
Ala Lys Ile Pro Thr Ser Leu His Arg Lys Trp Val Gly Leu Asn Leu
720 725 730

cag ttc ctc ctg gtc ttc ctc tgc atc ctg gtg caa atc gtc acc tgc 2679
Gln Phe Leu Leu Val Phe Leu Cys Ile Leu Val Gln Ile Val Thr Cys
735 740 745

atc atc tgg ctc tac acc gcg cct ccc tcc agc tac agg aac cat gag 2727
Ile Ile Trp Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg Asn His Glu
750 755 760

ctg gag gac gag gtc atc ttc atc acc tgc gac gag ggc tcg ctc atg 2775
Leu Glu Asp Glu Val Ile Phe Ile Thr Cys Asp Glu Gly Ser Leu Met
765 770 775

gcg ctg ggc ttc ctc atc ggc tac acc tgc ctc ctc gcc gcc atc tgc 2823
Ala Leu Gly Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys
780 785 790 795

ttc ttc ttc gcc ttc aag tcc cgt aag ctg ccg gag aac ttc aac gag 2871
Phe Phe Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn Glu
800 805 810

gct aag ttc atc acc ttc agc atg ttg atc ttc ttc atc gtc tgg atc 2919
Ala Lys Phe Ile Thr Phe Ser Met Leu Ile Phe Phe Ile Val Trp Ile
815 820 825

tcc ttc atc ccc gcc tat gtc agc acc tac ggc aag ttt gtg tcg gcc 2967
Ser Phe Ile Pro Ala Tyr Val Ser Thr Tyr Gly Lys Phe Val Ser Ala
830 835 840

gtg gag gtg att gcc atc ctg gcc tcc agc ttc ggg ctg ctg ggc tgc 3015
Val Glu Val Ile Ala Ile Leu Ala Ser Ser Phe Gly Leu Leu Gly Cys
845 850 855

att tac ttc aac aag tgt tac atc atc ctg ttc aag ccg tgc cgt aac 3063
Ile Tyr Phe Asn Lys Cys Tyr Ile Leu Phe Lys Pro Cys Arg Asn
860 865 870 875

acc atc gag gag gtg cgc tgc agc acg gcg gcc cac gcc ttc aag gtg 3111
Thr Ile Glu Glu Val Arg Cys Ser Thr Ala Ala His Ala Phe Lys Val
880 885 890

gcg gcc cgcc acc ctc cgg cgc agc gcg tct cgc aag cgc tcc 3159
Ala Ala Arg Ala Thr Leu Arg Arg Ser Ala Ala Ser Arg Lys Arg Ser
895 900 905

agc agc ctg tgc ggc tcc acc atc tcc tcg ccc gcc tcg tcc acc tgc 3207
Ser Ser Leu Cys Gly Ser Thr Ile Ser Ser Pro Ala Ser Ser Thr Cys
910 915 920

ggg ccg ggc ctc acc atg gag atg cag cgc tgc agc acg cag aag gtc	3255
Gly Pro Gly Leu Thr Met Glu Met Gln Arg Cys Ser Thr Gln Lys Val	
925 930 935	
agc ttc ggc agc ggc acc gtc acc ctg tcg ctc agc ttc gag gag aca	3303
Ser Phe Gly Ser Gly Thr Val Thr Leu Ser Leu Ser Phe Glu Glu Thr	
940 945 950 955	
ggc cga tac gcc acc ctc agc cgc acg gcc cgc agc agg aac tcg gcg	3351
Gly Arg Tyr Ala Thr Leu Ser Arg Thr Ala Arg Ser Arg Asn Ser Ala	
960 965 970	
gat ggc cgc agc ggc gac gac ctg cca tct aga cac cac gac cag ggc	3399
Asp Gly Arg Ser Gly Asp Asp Leu Pro Ser Arg His His Asp Gln Gly	
975 980 985	
ccg cct cag aaa tgc gag ccc cag ccc gcc aac gat gcc oga tac aag	3447
Pro Pro Gln Lys Cys Glu Pro Gln Pro Ala Asn Asp Ala Arg Tyr Lys	
990 995 1000	
gcg gcg ccg acc aag ggc acc cta gag tcg ccg ggc ggc agc aag gag	3495
Ala Ala Pro Thr Lys Gly Thr Leu Glu Ser Pro Gly Gly Ser Lys Glu	
1005 1010 1015	
cgc ccc aca act atg gag gaa acc taa tccaaactcct ccatcaaccc	3542
Arg Pro Thr Thr Met Glu Glu Thr *	
1020 1025	
caagaacatc ctccacggca gcaccgtcga caactgacat caactcctaa ccgggtggctg	3602
cccaacctct cccctctccg gcactttgcg ttttgctgaa gattgcagca tctgcagttc	3662
cttttatccc tgatttctg acttggatat ttactagtgt gcgtatggat atcacaacat	3722
aatgagttgc acaatttaggt gagcagagtt gtgtcaaagt atctgaacta tctgaagtat	3782
ctgaactact ttattctctc gaatttgtatt acaaacattt gaagtatttt tagtgacatt	3842
atgttctaactt attgtcaaga taatttgtta caacatataa ggtaccaccc gaagcagtga	3902
ctgagatgc cactgtgtatc acagaactgt ttatataacat ttatcattga aacctggatt	3962
gcaacagaaa tataatgact gtaacaaaaa aattgttgat tatctaaaa atgcaaaattg	4022
taatcagatg tgtaaaaattt gtaattactt ctgtacatata aatgcattt tcttgataaaa	4082
aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaagcggcc cgacagcaac gg	4134

Docket No.: 2856.1001-011
Title: "Polycation-Sensing Receptor ..."
Inventors: H. William Harris, *et al.*

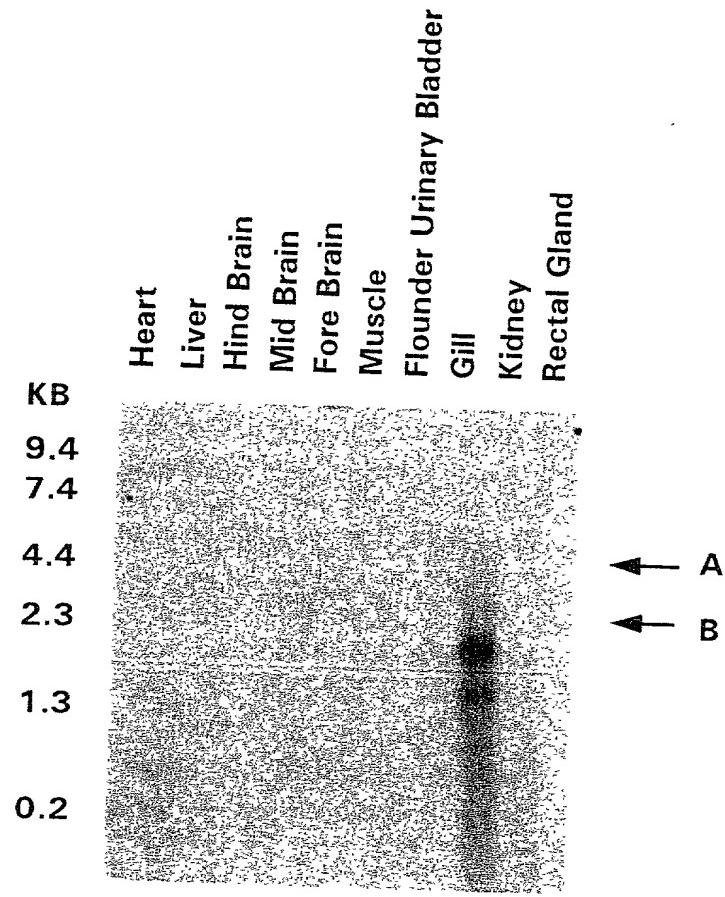


FIG. 6

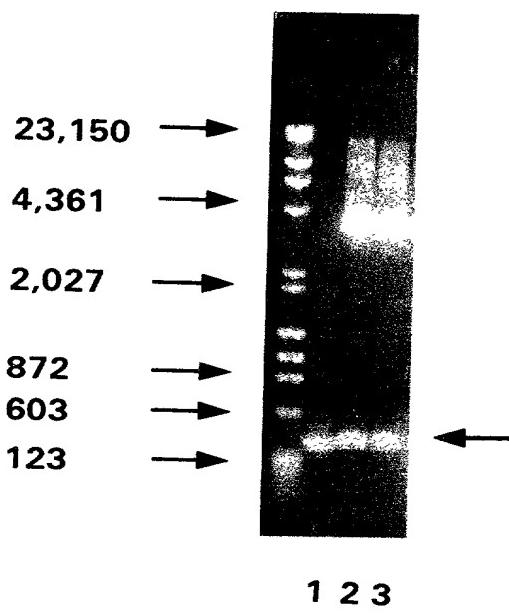


FIG. 7A



FIG. 7B

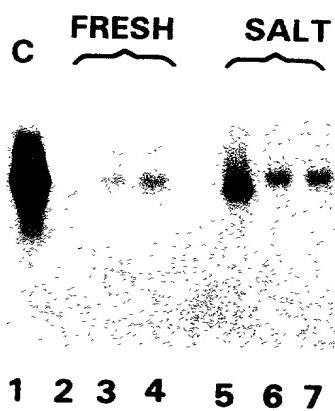


FIG.8

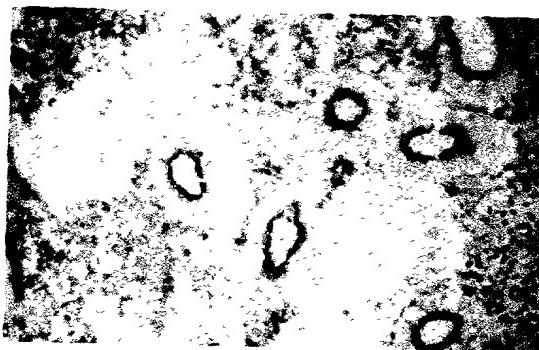


FIG.9A

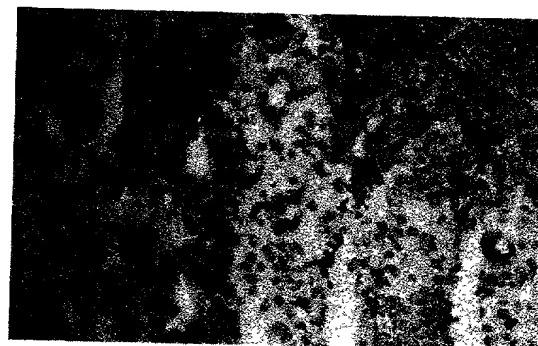


FIG.9B



FIG.9C

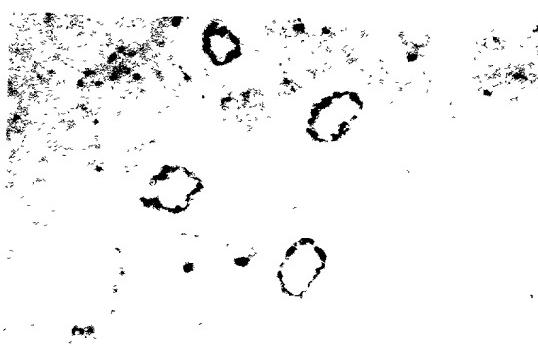


FIG.9D

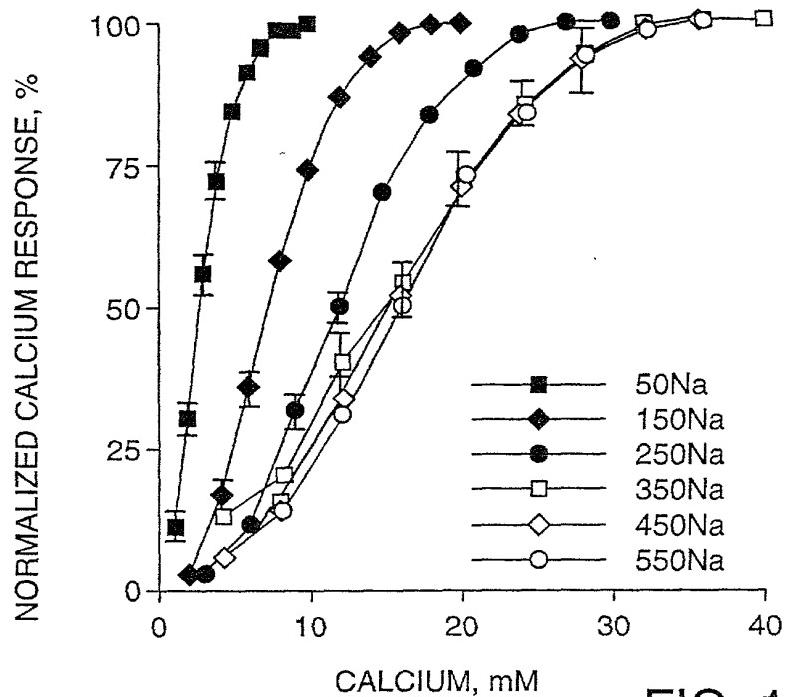


FIG. 10

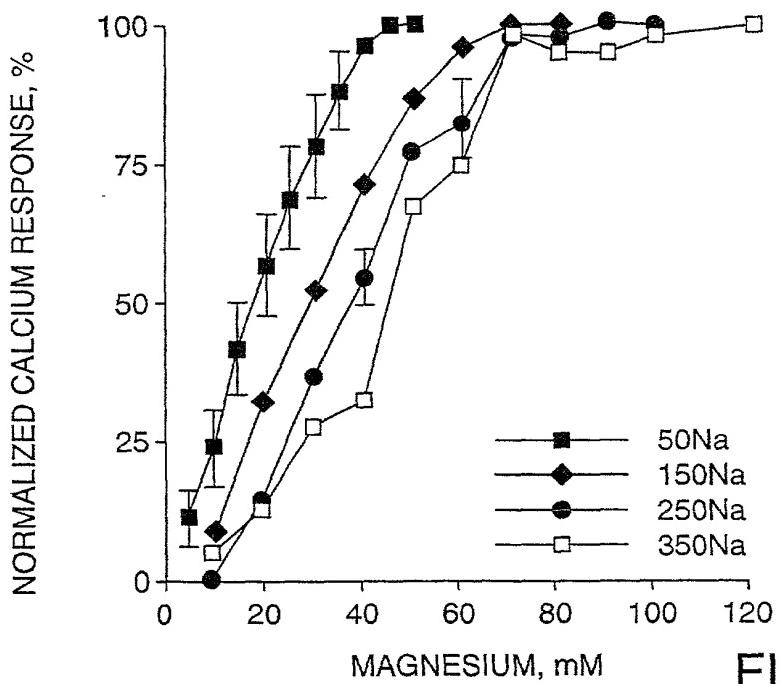


FIG. 11

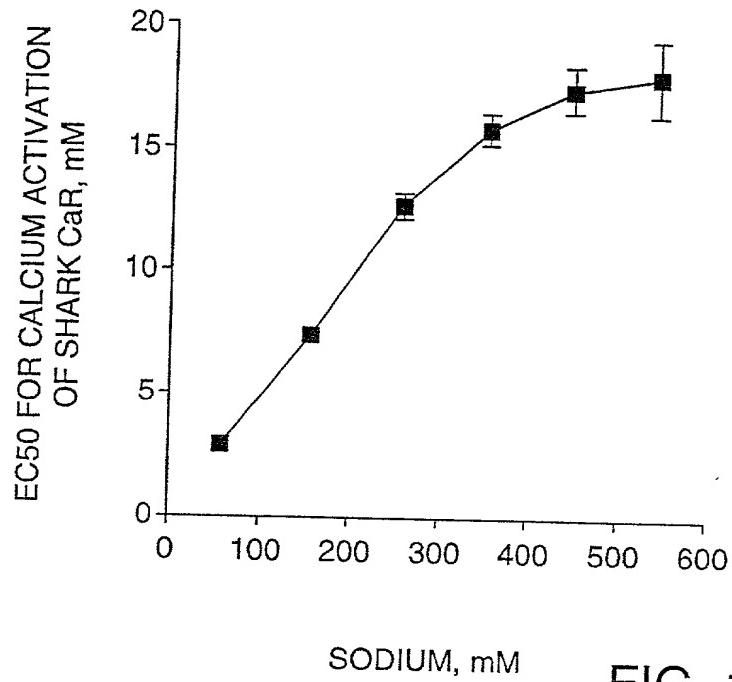


FIG. 12

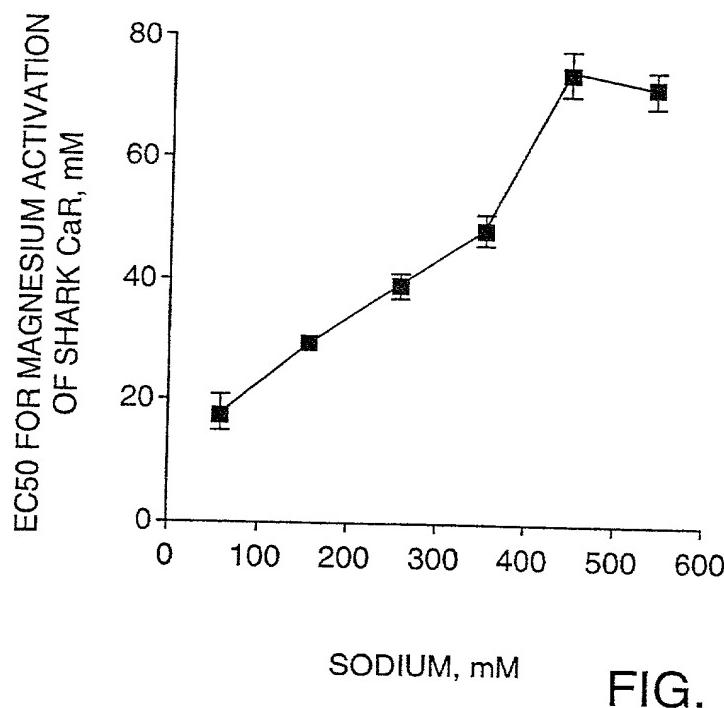


FIG. 13

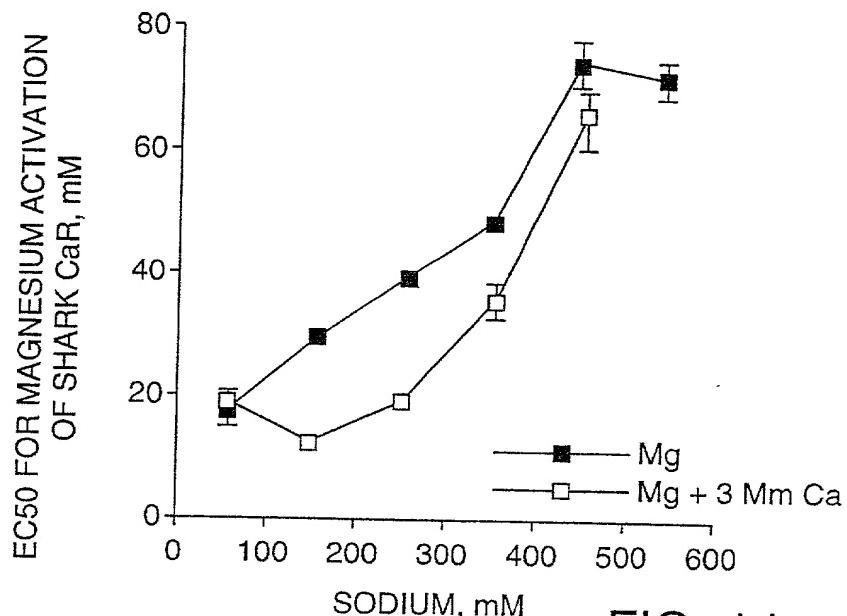
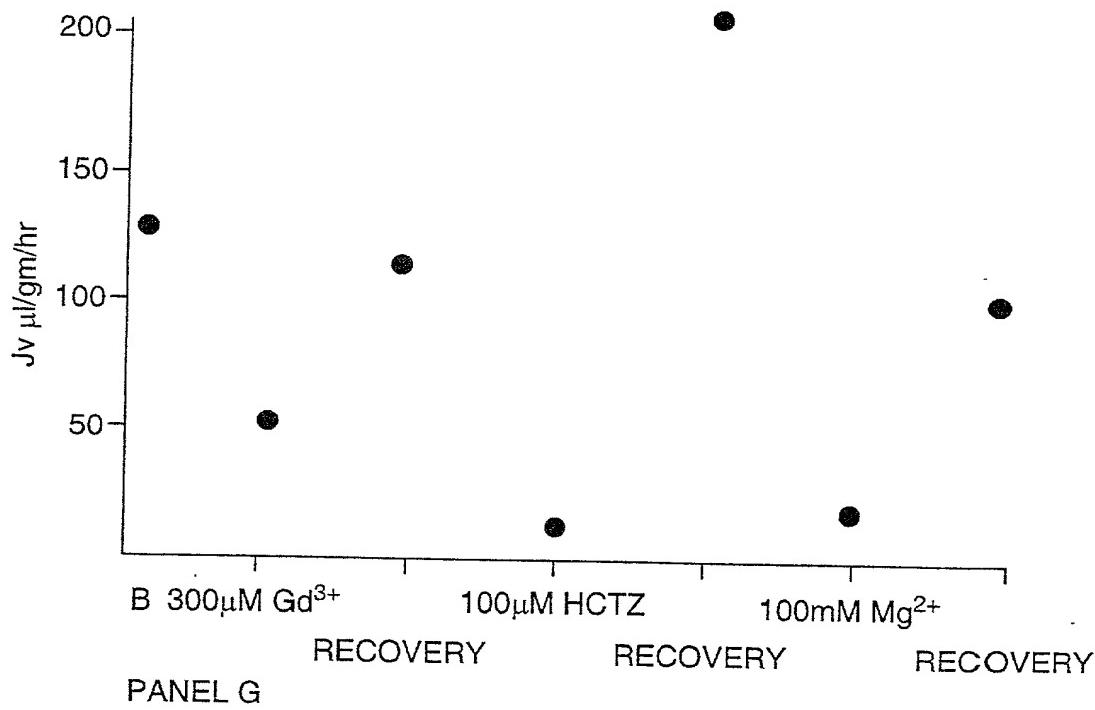


FIG. 14



PANEL G

FIG. 15

cta cta gtc ata tgg att gcg gcg gay gay gat tat ggc cgc cca ggg 48
Leu Leu Val Ile Trp Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly
1 5 10 15

ata gat aag ttt cga gaa gaa gct gaa gag agg gac atc tgc ata gat 96
Ile Asp Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp
20 25 30

ttc aat gag atg att tct cag tac tat aca caa aaa gag ctg gag ttt 144
Phe Asn Glu Met Ile Ser Gln Tyr Thr Gln Lys Glu Leu Glu Phe
35 40 45

att gca gat act att cag aat tcc tca gcc aaa gtg att gty gtc ttc 192
Ile Ala Asp Thr Ile Gln Asn Ser Ser Ala Lys Val Ile Xaa Val Phe
50 55 60

tca aat ggc cct gac ttg gaa cca cta ata caa gag ata gtt cga cgg 240
Ser Asn Gly Pro Asp Leu Glu Pro Leu Ile Gln Glu Ile Val Arg Arg
65 70 75 80

aac ata act gat aga ata tgg cta gca agt gaa gcg tgg gct agt tcc 288
Asn Ile Thr Asp Arg Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser
85 90 95

tca ctg ata gcc aaa cca gaa tac ttc cat gtt gtt ggt gga acc att 336
Ser Leu Ile Ala Lys Pro Glu Tyr Phe His Val Val Gly Gly Thr Ile
100 105 110

gga ttt gca cta aga gca gga cgc atc cca gga ttc cat gag ttt tta 384
Gly Phe Ala Leu Arg Ala Gly Arg Ile Pro Gly Phe His Glu Phe Leu
115 120 125

aaa aag gtc cat ccc agc agg tcc tcc cac aat ggc ttt gtc aag gaa 432
Lys Lys Val His Pro Ser Arg Ser Ser His Asn Gly Phe Val Lys Glu
130 135 140

ttc tgg gaa gaa aca ttt aat tgt tat ttc act gaa gaa tcc cta aca 480
Phe Trp Glu Glu Thr Phe Asn Cys Tyr Phe Thr Glu Glu Ser Leu Thr
145 150 155 160

caa cta aag aat tgc aaa aca cca acc cat gga tta gca atg cac aat 528
Gln Leu Lys Asn Cys Lys Thr Pro Thr His Gly Leu Ala Met His Asn
165 170 175

gac agt gcg aaa atg ggg cat tcc aca agg aca acg tta cga cct cca 576
Asp Ser Ala Lys Met Gly His Ser Thr Arg Thr Thr Leu Arg Pro Pro
180 185 190

FIG. 16A

tgc act gga gaa gag aat	atc acg agt gtg gag acc cct tac ctg gat	624	
Cys Thr Gly Glu Glu Asn Ile	Thr Ser Val Glu Thr Pro Tyr Leu Asp		
195	200	205	
tat act cac ctc cgt att tca tat aat gtg tat	gtg gca gtg tat tcg	672	
Tyr Thr His Leu Arg Ile Ser Tyr Asn Val	Tyr Val Ala Val Tyr Ser		
210	215	220	
att gct cac gct ctg cag gac atc tat gcc tgc	aca cct ggg aag ggg	720	
Ile Ala His Ala Leu Gln Asp Ile Tyr Ala Cys	Thr Pro Gly Lys Gly		
225	230	235	240
att ttt gcg aac gga tca tgt gcc gat atc aaa	aaa gtc gaa gcc tgg	768	
Ile Phe Ala Asn Gly Ser Cys Ala Asp Ile Lys	Lys Val Glu Ala Trp		
245	250	255	
aat cca tat gac tag t		784	
Asn Pro Tyr Asp *			
260			

FIG. 16B

Leu Leu Val Ile Trp Ile-Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly
1 5 10 15
Ile Asp Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp
20 25 30
Phe Asn Glu Met Ile Ser Gln Tyr Tyr Thr Gln Lys Glu Leu Glu Phe
35 40 45
Ile Ala Asp Thr Ile Gln Asn Ser Ser Ala Lys Val Ile Val Val Phe
50 55 60
Ser Asn Gly Pro Asp Leu Glu Pro Leu Ile Gln Glu Ile Val Arg Arg
65 70 75 80
Asn Ile Thr Asp Arg Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser
85 90 95
Ser Leu Ile Ala Lys Pro Glu Tyr Phe His Val Val Gly Gly Thr Ile
100 105 110
Gly Phe Ala Leu Arg Ala Gly Arg Ile Pro Gly Phe His Glu Phe Leu
115 120 125
Lys Lys Val His Pro Ser Arg Ser Ser His Asn Gly Phe Val Lys Glu
130 135 140
Phe Trp Glu Glu Thr Phe Asn Cys Tyr Phe Thr Glu Glu Ser Leu Thr
145 150 155 160
Gln Leu Lys Asn Cys Lys Thr Pro Thr His Gly Leu Ala Met His Asn
165 170 175
Asp Ser Ala Lys Met Gly His Ser Thr Arg Thr Thr Leu Arg Pro Pro
180 185 190
Cys Thr Gly Glu Glu Asn Ile Thr Ser Val Glu Thr Pro Tyr Leu Asp
195 200 205
Tyr Thr His Leu Arg Ile Ser Tyr Asn Val Tyr Val Ala Val Tyr Ser
210 215 220
Ile Ala His Ala Leu Gln Asp Ile Tyr Ala Cys Thr Pro Gly Lys Gly
225 230 235 240
Ile Phe Ala Asn Gly Ser Cys Ala Asp Ile Lys Lys Val Glu Ala Trp
245 250 255
Asn Pro Tyr Asp
260

10 20 30 40 50
* * * * *
CTA CTA GTC ATA TGG ATT GCG GCG GAY GAY GAT TAT GGC CGC CCA GGG ATA GAT
GAT GAT CAG TAT ACC TAA CGC CGC CTR CTR CTA ATA CCG GCG GGT CCC TAT CTA
Leu Leu Val Ile Trp Ile Ala Ala Asp Asp Asp Asp Tyr Gly Arg Pro Gly Ile Asp>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

60 70 80 90 100
* * * * *
AAG TTT CGA GAA GAA GCT GAA GAG AGG GAC ATC TGC ATA GAT TTC AAT GAG ATG
TTC AAA GCT CTT CTT CGA CTT CTC TCC CTG TAG ACG TAT CTA AAG TTA CTC TAC
Lys Phe Arg Glu Glu Ala Glu Arg Asp Ile Cys Ile Asp Phe Asn Glu Met>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

110 120 130 140 150 160
* * * * * *
ATT TCT CAG TAC TAT ACA CAA AAA GAG CTG GAG TTT ATT GCA GAT ACT ATT CAG
TAA AGA GTC ATG ATA TGT GTT TTT CTC GAC CTC AAA TAA CGT CTA TGA TAA GTC
Ile Ser Gln Tyr Tyr Thr Gln Lys Glu Leu Glu Phe Ile Ala Asp Thr Ile Gln>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

170 180 190 200 210
* * * * *
AAT TCC TCA GCC AAA GTG ATT GTY GTC TTC TCA AAT GGC CCT GAC TTG GAA CCA
TTA AGG AGT CGG TTT CAC TAA CAR CAG AAG AGT TTA CCG GGA CTG AAC CTT GGT
Asn Ser Ser Ala Lys Val Ile Val Val Phe Ser Asn Gly Pro Asp Leu Glu Pro>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

220 230 240 250 260 270
* * * * * *
CTA ATA CAA GAG ATA GTT CGA CGG AAC ATA ACT GAT AGA ATA TGG CTA GCA AGT
GAT TAT GTT CTC TAT CAA GCT GCC TTG TAT TGA CTA TCT TAT ACC GAT CGT TCA
Leu Ile Gln Glu Ile Val Arg Arg Asn Ile Thr Asp Arg Ile Trp Leu Ala Ser>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

280 290 300 310 320
* * * * *
GAA GCG TGG GCT AGT TCC TCA CTG ATA GCC AAA CCA GAA TAC TTC CAT GTT GTT
CTT CGC ACC CGA TCA AGG AGT GAC TAT CGG TTT GGT CTT ATG AAG GTA CAA CAA
Glu Ala Trp Ala Ser Ser Leu Ile Ala Lys Pro Glu Tyr Phe His Val Val>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

330 340 350 360 370
* * * * *
GGT GGA ACC ATT GGA TTT GCA CTA AGA GCA GGA CGC ATC CCA GGA TTC CAT GAG
CCA CCT TGG TAA CCT AAA CGT GAT TCT CGT CCT GCG TAG GGT CCT AAG GTA CTC
Gly Gly Thr Ile Gly Phe Ala Leu Arg Ala Gly Arg Ile Pro Gly Phe His Glu>
____o____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

380 390 400 410 420 430
* * * * * *
TTT TTA AAA AAG GTC CAT CCC AGC AGG TCC TCC CAC AAT GGC TTT GTC AAG GAA
AAA AAT TTT TTC CAG GTA GGG TCG TCC AGG AGG GTG TTA CCG AAA CAG TTC CTT
Phe Leu Lys Lys Val His Pro Ser Arg Ser His Asn Gly Phe Val Lys Glu>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

440 450 460 470 480
* * * * *
TTC TGG GAA GAA ACA TTT AAT TGT TAT TTC ACT GAA GAA TCC CTA ACA CAA CTA
AAG ACC CTT CTT TGT AAA TTA ACA ATA AAG TGA CTT CTT AGG GAT TGT GTT GAT
Phe Trp Glu Glu Thr Phe Asn Cys Tyr Phe Thr Glu Glu Ser Leu Thr Gln Leu>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

490 500 510 520 530 540

* * * * *

AAG AAT TGC AAA ACA CCA ACC CAT GGA TTA GCA ATG CAC AAT GAC AGT GCG AAA
TTC TTA ACG TTT TGT GGT TGG GTA CCT AAT CGT TAC GTG TTA CTG TCA CGC TTT
Lys Asn Cys Lys Thr Pro Thr His Gly Leu Ala Met His Asn Asp Ser Ala Lys>
____a____a____a____a____a____a____ORF RF[1] ____a____a____a____a____a____a____>

550 560 570 580 590

* * * * *

ATG GGG CAT TCC ACA AGG ACA ACG TTA CGA CCT CCA TGC ACT GGA GAA GAG AAT
TAC CCC GTA AGG TGT TCC TGT TGC AAT GCT GGA GGT ACG TGA CCT CTT CTC TTA
Met Gly His Ser Thr Arg Thr Thr Leu Arg Pro Pro Cys Thr Gly Glu Glu Asn>
____a____a____a____a____a____a____a____ORF RF[1] ____a____a____a____a____a____a____>

600 610 620 630 640

* * * * *

ATC ACG AGT GTG GAG ACC CCT TAC CTG GAT TAT ACT CAC CTC CGT ATT TCA TAT
TAG TGC TCA CAC CTC TGG GGA ATG GAC CTA ATA TGA GTG GAG GCA TAA AGT ATA
Ile Thr Ser Val Glu Thr Pro Tyr Leu Asp Tyr Thr His Leu Arg Ile Ser Tyr>
____a____a____a____a____a____a____a____ORF RF[1] ____a____a____a____a____a____a____>

650 660 670 680 690 700

* * * * *

AAT GTG TAT GTG GCA GTG TAT TCG ATT GCT CAC GCT CTG CAG GAC ATC TAT GCC
TTA CAC ATA CAC CGT CAC ATA AGC TAA CGA GTG CGA GAC GTC CTG TAG ATA CGG
Asn Val Tyr Val Ala Val Tyr Ser Ile Ala His Ala Leu Gln Asp Ile Tyr Ala>
____a____a____a____a____a____a____a____ORF RF[1] ____a____a____a____a____a____a____>

710 720 730 740 750

* * * * *

TGC ACA CCT GGG AAG GGG ATT TTT GCG AAC GGA TCA TGT GCC GAT ATC AAA AAA
ACG TGT GGA CCC TTC CCC TAA AAA CGC TTG CCT AGT ACA CGG CTA TAG TTT TTT
Cys Thr Pro Gly Lys Gly Ile Phe Ala Asn Gly Ser Cys Ala Asp Ile Lys Lys>
____a____a____a____a____a____a____a____ORF RF[1] ____a____a____a____a____a____a____>

760 770 780

* * *

GTC GAA GCC TGG AAT CCA TAT GAC TAGT
CAG CTT CGG ACC TTA GGT ATA CTG ATCA
Val Glu Ala Trp Asn Pro Tyr Asp>
____a____a____ORF RF[1] ____a____a____>

tt ctg aca ata ttt gct gtg cta gga ata ctg atc act tcc ttt gtt 47
Leu Thr Ile Phe Ala Val Leu Gly Ile Leu Ile Thr Ser Phe Val
1 5 10 15

ttg gga gta ttc att aag ttc aga aat act cct att gtg aaa gcc act 95
Leu Gly Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val Lys Ala Thr
20 25 30

aac aga gaa ctc tcc tat ctc ctc ttc tcc tta atc tgc tgt ttc 143
Asn Arg Glu Leu Ser Tyr Leu Leu Phe Ser Leu Ile Cys Cys Phe
35 40 45

tcc agc tca ttg atc ttc att gga gaa ccc aaa gat tgg acc tgc aga 191
Ser Ser Ser Leu Ile Phe Ile Gly Glu Pro Lys Asp Trp Thr Cys Arg
50 55 60

ctg cgt caa cct gca ttt gga atc agc ttt gtg ctg tgc att tct tgc 239
Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile Ser Cys
65 70 75

att ctg gtg aaa act aat cgt gtg cta ttg gtc ttt gag gcc aag atc 287
Ile Leu Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu Ala Lys Ile
80 85 90 95

cca act agc ctc cat cga aag tgg gtg ggc ctc aat ttg caa ttc tta 335
Pro Thr Ser Leu His Arg Lys Trp Val Gly Leu Asn Leu Gln Phe Leu
100 105 110

ctg gtt ttc ctc tgt att ctt gtg caa att gtt act tgt gtc atc tgg 383
Leu Val Phe Leu Cys Ile Leu Val Gln Ile Val Thr Cys Val Ile Trp
115 120 125

ctt tac aca gca ccc cct tcg agc tac aga aat cat gaa cta gaa gat 431
Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg Asn His Glu Leu Glu Asp
130 135 140

gaa atc att ttt att aca tgt gat gaa ggt tcc tta atg gca ctt ggt 479
Glu Ile Ile Phe Ile Thr Cys Asp Glu Gly Ser Leu Met Ala Leu Gly
145 150 155

ttt ctc att ggt tac aca tgc ctc ctt gct gcc att tgc ttc ttt ttt 527
Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Phe
160 165 170 175

gcc ttt aag tct cgc aaa ctc cca gag aac ttc aat gag gcc aaa ttt 575
Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala Lys Phe
180 185 190

att acc ttc agc atg ctg ata tt 598
Ile Thr Phe Ser Met Leu Ile
195

Leu Thr Ile Phe Ala Val Leu Gly Ile Leu Ile Thr Ser Phe Val Leu
1 5 10 15
Gly Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn
20 25 30
Arg Glu Leu Ser Tyr Leu Leu Phe Ser Leu Ile Cys Cys Phe Ser
35 40 45
Ser Ser Leu Ile Phe Ile Gly Glu Pro Lys Asp Trp Thr Cys Arg Leu
50 55 60
Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile Ser Cys Ile
65 70 75 80
Leu Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu Ala Lys Ile Pro
85 90 95
Thr Ser Leu His Arg Lys Trp Val Gly Leu Asn Leu Gln Phe Leu Leu
100 105 110
Val Phe Leu Cys Ile Leu Val Gln Ile Val Thr Cys Val Ile Trp Leu
115 120 125
Tyr Thr Ala Pro Pro Ser Ser Tyr Arg Asn His Glu Leu Glu Asp Glu
130 135 140
Ile Ile Phe Ile Thr Cys Asp Glu Gly Ser Leu Met Ala Leu Gly Phe
145 150 155 160
Leu Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Phe Ala
165 170 175
Phe Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala Lys Phe Ile
180 185 190
Thr Phe Ser Met Leu Ile
195

10 20 30 40 50
* * * * *

TT CTG ACA ATA TTT GCT GTG CTA GGA ATA CTG ATC ACT TCC TTT GTT TTG GGA
AA GAC TGT TAT AAA CGA CAC GAT CCT TAT GAC TAG TGA AGG AAA CAA AAC CCT
Leu Thr Ile Phe Ala Val Leu Gly Ile Leu Ile Thr Ser Phe Val Leu Gly>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

60 70 80 90 100
* * * * *

GTA TTC ATT AAG TTC AGA AAT ACT CCT ATT GTG AAA GCC ACT AAC AGA GAA CTC
CAT AAG TAA TTC AAG TCT TTA TGA GGA TAA CAC TTT CGG TGA TTG TCT CTT GAG
Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn Arg Glu Leu>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

110 120 130 140 150 160
* * * * *

TCC TAT CTC CTC TTC TCC TTA ATC TGC TGT TTC TCC AGC TCA TTG ATC TTC
AGG ATA GAG GAG AAG AGG AAT TAG ACG ACA AAG AGG TCG AGT AAC TAG AAG
Ser Tyr Leu Leu Phe Ser Leu Ile Cys Cys Phe Ser Ser Ser Leu Ile Phe>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

170 180 190 200 210
* * * * *

ATT GGA GAA CCC AAA GAT TGG ACC TGC AGA CTG CGT CAA CCT GCA TTT GGA ATC
TAA CCT CTT GGG TTT CTA ACC TGG ACG TCT GAC GCA GTT GGA CGT AAA CCT TAG
Ile Gly Glu Pro Lys Asp Trp Thr Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

220 230 240 250 260
* * * * *

AGC TTT GTG CTG TGC ATT TCT TGC ATT CTG GTG AAA ACT AAT CGT GTG CTA TTG
TCG AAA CAC GAC ACG TAA AGA ACG TAA GAC CAC TTT TGA TTA GCA CAC GAT AAC
Ser Phe Val Leu Cys Ile Ser Cys Ile Leu Val Lys Thr Asn Arg Val Leu Leu>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

270 280 290 300 310 320
* * * * *

GTC TTT GAG GCC AAG ATC CCA ACT AGC CTC CAT CGA AAG TGG GTG GGC CTC AAT
CAG AAA CTC CGG TTC TAG GGT TGA TCG GAG GTA GCT TTC ACC CAC CCG GAG TTA
Val Phe Glu Ala Lys Ile Pro Thr Ser Leu His Arg Lys Trp Val Gly Leu Asn>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

330 340 350 360 370
* * * * *

TTG CAA TTC TTA CTG GTT TTC CTC TGT ATT CTT GTG CAA ATT GTT ACT TGT GTC
AAC GTT AAG AAT GAC CAA AAG GAG ACA TAA GAA CAC GTT TAA CAA TGA ACA CAG
Leu Gln Phe Leu Leu Val Phe Leu Cys Ile Leu Val Gln Ile Val Thr Cys Val>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

380 390 400 410 420 430
* * * * *

ATC TGG CTT TAC ACA GCA CCC CCT TCG AGC TAC AGA AAT CAT GAA CTA GAA GAT
TAG ACC GAA ATG TGT CGT GGG GGA AGC TCG ATG TCT TTA GTA CTT GAT CTT CTA
Ile Trp Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg Asn His Glu Leu Glu Asp>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

440 450 460 470 480
* * * * *

GAA ATC ATT TTT ATT ACA TGT GAT GAA GGT TCC TTA ATG GCA CTT GGT TTT CTC
CTT TAG TAA AAA TAA TGT ACA CTA CTT CCA AGG AAT TAC CGT GAA CCA AAA GAG
Glu Ile Ile Phe Ile Thr Cys Asp Glu Gly Ser Leu Met Ala Leu Gly Phe Leu>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

Docket No.: 2856.1001-011
Title: "Polycation-Sensing Receptor..."
Inventors: H. William Harris, et al.

490 500 510 520 530
* * * * *
ATT GGT TAC ACA TGC CTC CTT GCT GCC ATT TGC TTC TTT GCC TTT AAG TCT
TAA CCA ATG TGT ACG GAG GAA CGA CGG TAA ACG AAG AAA AAA CGG AAA TTC AGA
Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Phe Ala Phe Lys Ser>
____a____a____a____a____a____a____a____ORF RF[3] ____a____a____a____a____a____a____>

540 550 560 570 580 590
* * * * * *
CGC AAA CTC CCA GAG AAC TTC AAT GAG GCC AAA TTT ATT ACC TTC AGC ATG CTG
GCG TTT GAG GGT CTC TTG AAG TTA CTC CGG TTT AAA TAA TGG AAG TCG TAC GAC
Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala Lys Phe Ile Thr Phe Ser Met Leu>
____a____a____a____a____a____a____a____a____a____a____a____a____>

ATA TT
TAT AA
Ile>
____>

1001-011-2003

g ttg acc ata tgt gca g^tg ctg ggt gtt gcc ytg acg ggc ttc qtg atg 49
Leu Thr Ile Cys Ala Val Leu Gly Val Ala Xaa Thr Gly Phe Val Met
1 5 10 15

gcc gtc ttt gtc cga ttc cgc aac acc cca ata gtg aaa gcc acg aac 97
Ala Val Phe Val Arg Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn
20 25 30

cga gaa ctg tcc tac gtc ctc ctg ttc tct ctc atc tgt tgc ttc tcc 145
Arg Glu Leu Ser Tyr Val Leu Leu Phe Ser Leu Ile Cys Cys Phe Ser
35 40 45

agc tcc ctc atc ttc ata gga gag ccg cag gat tgg atg tgc cgc tta 193
Ser Ser Leu Ile Phe Ile Gly Glu Pro Gln Asp Trp Met Cys Arg Leu
50 55 60

cgc caa ccg gcc ttt ggg atc agt ttt gtt ctc tgt atc tcg tgc atc 241
Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile Ser Cys Ile
65 70 75 80

ctt gtg aaa aca aac cka gtc ctc ttg gtg ttt gaa gcc aag atc ccg 289
Leu Val Lys Thr Asn Xaa Val Leu Val Phe Glu Ala Lys Ile Pro
85 90 95

aca agt ctc cat cgt aaa tgg tgg ggg tta aac cta cag ttc ctg ctg 337
Thr Ser Leu His Arg Lys Trp Trp Gly Leu Asn Leu Gln Phe Leu Leu
100 105 110

gtg ttt ctg tgc aca ttt gtc caa gtc atg ata tgt gtg gtc tgg ctg 385
Val Phe Leu Cys Thr Phe Val Gln Val Met Ile Cys Val Val Trp Leu
115 120 125

tac aac gcc cca cct tcc agt tac agg aat tat gac ata gat gag atg 433
Tyr Asn Ala Pro Pro Ser Ser Tyr Arg Asn Tyr Asp Ile Asp Glu Met
130 135 140

att ttt atc aca tgt aat gaa ggc tct gta atg gct ctt ggg ttt ctt 481
Ile Phe Ile Thr Cys Asn Glu Gly Ser Val Met Ala Leu Gly Phe Leu
145 150 155 160

att ggc tat aca tgc ctg ctg gcc gct ata tgt ttc ttc ttt gca ttc 529
Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Ala Phe
165 170 175

aaa tca cgg aaa ctt cca gaa aac ttc acc gag gct aag ttc atc act 577
Lys Ser Arg Lys Leu Pro Glu Asn Phe Thr Glu Ala Lys Phe Ile Thr
180 185 190

ttt agt atg ctc ata tt 594
Phe Ser Met Leu Ile
195

Leu Thr Ile Cys Ala Val Leu Gly Val Ala Leu Thr Gly Phe Val Met
1 5 10 15
Ala Val Phe Val Arg Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn
20 25 30
Arg Glu Leu Ser Tyr Val Leu Leu Phe Ser Leu Ile Cys Cys Phe Ser
35 40 45
Ser Ser Leu Ile Phe Ile Gly Glu Pro Gln Asp Trp Met Cys Arg Leu
50 55 60
Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile Ser Cys Ile
65 70 75 80
Leu Val Lys Thr Asn Xaa Val Leu Leu Val Phe Glu Ala Lys Ile Pro
85 90 95
Thr Ser Leu His Arg Lys Trp Trp Gly Leu Asn Leu Gln Phe Leu Leu
100 105 110
Val Phe Leu Cys Thr Phe Val Gln Val Met Ile Cys Val Val Trp Leu
115 120 125
Tyr Asn Ala Pro Pro Ser Ser Tyr Arg Asn Tyr Asp Ile Asp Glu Met
130 135 140
Ile Phe Ile Thr Cys Asn Glu Gly Ser Val Met Ala Leu Gly Phe Leu
145 150 155 160
Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Phe Ala Phe
165 170 175
Lys Ser Arg Lys Leu Pro Glu Asn Phe Thr Glu Ala Lys Phe Ile Thr
180 185 190
Phe Ser Met Leu Ile
195

10 * 20 * 30 * 40 * 50 *

G TTG ACC ATA TGT GCA GTG CTG GGT GTT GCC YTG ACG GGC TTC GTG ATG GCC
C AAC TGG TAT ACA CGT CAC GAC CCA CAA CGG RAC TGC CCG AAG CAC TAC CGG
Leu Thr Ile Cys Ala Val Leu Gly Val Ala Leu Thr Gly Phe Val Met Ala>
____a____a____a____a____a____ORF RF[2] ____a____a____a____a____a____a____>

60 * 70 * 80 * 90 * 100 *

GTC TTT GTC CGA TTC CGC AAC ACC CCA ATA GTG AAA GCC ACG AAC CGA GAA CTG
CAG AAA CAG GCT AAG GCG TTG TGG GGT TAT CAC TTT CGG TGC TTG GCT CTT GAC
Val Phe Val Arg Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn Arg Glu Leu>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

110 * 120 * 130 * 140 * 150 * 160 *

TCC TAC GTC CTC CTG TTC CTC ATC TGT TGC TTC TCC AGC TCC CTC ATC TTC
AGG ATG CAG GAG GAC AAG AGA GAG TAG ACA ACG AAG AGG TCG AGG GAG TAG AAG
Ser Tyr Val Leu Leu Phe Ser Leu Ile Cys Cys Phe Ser Ser Ser Leu Ile Phe>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

170 * 180 * 190 * 200 * 210 *

ATA GGA GAG CCG CAG GAT TGG ATG TGC CGC TTA CGC CAA CCG GCC TTT GGG ATC
TAT CCT CTC GGC GTC CTA ACC TAC ACG GCG AAT GCG GTT GGC CGG AAA CCC TAG
Ile Gly Glu Pro Gln Asp Trp Met Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

220 * 230 * 240 * 250 * 260 *

AGT TTT GTT CTC TGT ATC TCG TGC ATC CTT GTG AAA ACA AAC CKA GTC CTC TTG
TCA AAA CAA GAG ACA TAG AGC ACG TAG GAA CAC TTT TGT TTG GMT CAG GAG AAC
Ser Phe Val Leu Cys Ile Ser Cys Ile leu Val Lys Thr Asn Xxx Val Leu Leu>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

270 * 280 * 290 * 300 * 310 * 320 *

GTG TTT GAA GCC AAG ATC CCG ACA AGT CTC CAT CGT AAA TGG TGG GGG TTA AAC
CAC AAA CTT CGG TTC TAG GGC TGT TCA GAG GTA GCA TTT ACC ACC CCC AAT TTG
Val Phe Glu Ala Lys Ile Pro Thr Ser Leu His Arg Lys Trp Trp Gly Leu Asn>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

330 * 340 * 350 * 360 * 370 *

CTA CAG TTC CTG CTG GTG TTT CTG TGC ACA TTT GTC CAA GTC ATG ATA TGT GTG
GAT GTC AAG GAC GAC CAC AAA GAC ACG TGT AAA CAG GTT CAG TAC TAT ACA CAC
Leu Gln Phe Leu Leu Val Phe Leu Cys Thr Phe Val Gln Val Met Ile Cys Val>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

380 * 390 * 400 * 410 * 420 * 430 *

GTC TGG CTG TAC AAC GCC CCA CCT TCC AGT TAC AGG AAT TAT GAC ATA GAT GAG
CAG ACC GAC ATG TTG CGG GGT GGA AGG TCA ATG TCC TTA ATA CTG TAT CTA CTC
Val Trp Leu Tyr Asn Ala Pro Pro Ser Ser Tyr Arg Asn Tyr Asp Ile Asp Glu>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

440 * 450 * 460 * 470 * 480 *

ATG ATT TTT ATC ACA TGT AAT GAA GGC TCT GTA ATG GCT CTT GGG TTT CTT ATT
TAC TAA AAA TAG TGT ACA TTA CTT CCG AGA CAT TAC CGA GAA CCC AAA GAA TAA
Met Ile Phe Ile Thr Cys Asn Glu Gly Ser Val Met Ala Leu Gly Phe Leu Ile>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

Docket No.: 2856.1001-011
Title: "Polycation-Sensing Receptor ..."
Inventors: H. William Harris, et al.

490 500 510 520 530
* * * * *
GGC TAT ACA TGC CTG GCC GCT ATA TGT TTC TTT GCA TTC AAA TCA CGG
CCG ATA TGT ACG GAC GAC CGG CGA TAT ACA AAG AAG AAA CGT AAG TTT AGT GCC
Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Phe Ala Phe Lys Ser Arg>
____a____a____a____a____a____a____ORF RF[2] ____a____a____a____a____a____a____>

540 550 560 570 580 590
* * * * * *
AAA CTT CCA GAA AAC TTC ACC GAG GCT AAG TTC ATC ACT TTT AGT ATG CTC ATA
TTT GAA GGT CTT TTG AAG TGG CTC CGA TTC AAG TAG TGA AAA TCA TAC GAG TAT
Lys Leu Pro Glu Asn Phe Thr Glu Ala Lys Phe Ile Thr Phe Ser Met Leu Ile>
____a____a____a____a____a____a____ORF RF[2] ____a____a____a____a____a____a____>

TT
AA

100165496 464.000

tg tcg tgg acg gag ccc ttt ggg atc gcg ttg gcc ata tgt gca gcg	47
Ser Trp Thr Glu Pro Phe Gly Ile Ala Leu Ala Ile Cys Ala Ala	
1 5 10 15	
ctg ggt gtt gcc ttg acg ggc ttc gtg atg gcc gtc ttt atc aga ttc	95
Leu Gly Val Ala Leu Thr Gly Phe Val Met Ala Val Phe Ile Arg Phe	
20 25 30	
cgc aac acc cca ata gtg aag gcc acg aac cga gaa ctg tcc tat gtc	143
Arg Asn Thr Pro Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Val	
35 40 45	
ctc ctg ttc tct ctc atc tgt tgc ttc agt tcc ctc atc ttt att	191
Leu Leu Phe Ser Leu Ile Cys Cys Phe Ser Ser Leu Ile Phe Ile	
50 55 60	
gga gag ccg cag gat tgg atg tgt cgt tta cgc caa cct gcc ttt ggg	239
Gly Glu Pro Gln Asp Trp Met Cys Arg Leu Arg Gln Pro Ala Phe Gly	
65 70 75	
atc agt ttt gtt ctc tgt atc tcc tgc atc ctt gtg aaa act aat aga	287
Ile Ser Phe Val Leu Cys Ile Ser Cys Ile Leu Val Lys Thr Asn Arg	
80 85 90 95	
gta ctc tta gta ttt gaa gcc aag atc ccc aca agt ctc cat cgt aaa	335
Val Leu Leu Val Phe Glu Ala Lys Ile Pro Thr Ser Leu His Arg Lys	
100 105 110	
tgg tgg ggg tta aac ctt cag ttt ttg ctg gtg ttt ctg tgc aca ttt	383
Trp Trp Gly Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys Thr Phe	
115 120 125	
gtc caa gtc atg atc tgt gtt gtc tgg ctg tac aat gcc cct ccc tcc	431
Val Gln Val Met Ile Cys Val Val Trp Leu Tyr Asn Ala Pro Pro Ser	
130 135 140	
agt tac agg aat tat gac ata gat gag atg att ttt atc aca	473
Ser Tyr Arg Asn Tyr Asp Ile Asp Glu Met Ile Phe Ile Thr	
145 150 155	
tg	475

Ser Trp Thr Glu Pro Phe Gly Ile Ala Leu Ala Ile Cys Ala Ala Leu
1 5 10 15
Gly Val Ala Leu Thr Gly Phe Val Met Ala Val Phe Ile Arg Phe Arg
20 25 30
Asn Thr Pro Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Val Leu
35 40 45
Leu Phe Ser Leu Ile Cys Cys Phe Ser Ser Ser Leu Ile Phe Ile Gly
50 55 60
Glu Pro Gln Asp Trp Met Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile
65 70 75 80
Ser Phe Val Leu Cys Ile Ser Cys Ile Leu Val Lys Thr Asn Arg Val
85 90 95
Leu Leu Val Phe Glu Ala Lys Ile Pro Thr Ser Leu His Arg Lys Trp
100 105 110
Trp Gly Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys Thr Phe Val
115 120 125
Gln Val Met Ile Cys Val Val Trp Leu Tyr Asn Ala Pro Pro Ser Ser
130 135 140
Tyr Arg Asn Tyr Asp Ile Asp Glu Met Ile Phe Ile Thr
145 150 155

FIG. 26

10 20 30 40 50
* * * * *
TG TCG TGG ACG GAG CCC TTT GGG ATC GCG TTG GCC ATA TGT GCA GCG CTG GGT
AC AGC ACC TGC CTC GGG AAA CCC TAG CGC AAC CGG TAT ACA CGT CGC GAC CCA
Ser Trp Thr Glu Pro Phe Gly Ile Ala Leu Ala Ile Cys Ala Ala Leu Gly>
____a____a____a____a____a____a____ORF RF[3] ____a____a____a____a____a____a____>

60 70 80 90 100
* * * * *
GTT GCC TTG ACG GGC TTC GTG ATG GCC GTC TTT ATC AGA TTC CGC AAC ACC CCA
CAA CGG AAC TGC CCG AAG CAC TAC CGG CAG AAA TAG TCT AAG GCG TTG TGG GGT
Val Ala Leu Thr Gly Phe Val Met Ala Val Phe Ile Arg Phe Arg Asn Thr Pro>
____a____a____a____a____a____a____a____ORF RF[3] ____a____a____a____a____a____a____>

110 120 130 140 150 160
* * * * * *
ATA GTG AAG GCC ACG AAC CGA GAA CTG TCC TAT GTC CTC CTG TTC TCT CTC ATC
TAT CAC TTC CGG TGC TTG GCT CTT GAC AGG ATA CAG GAG GAC AAG AGA GAG TAG
Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Val Leu Leu Phe Ser Leu Ile>
____a____a____a____a____a____a____a____a____ORF RF[3] ____a____a____a____a____a____a____>

170 180 190 200 210
* * * * *
TGT TGC TTC TCC AGT TCC CTC ATC TTT ATT GGA GAG CCG CAG GAT TGG ATG TGT
ACA ACG AAG AGG TCA AGG GAG TAG AAA TAA CCT CTC GGC GTC CTA ACC TAC ACA
Cys Cys Phe Ser Ser Leu Ile Phe Ile Gly Glu Pro Gln Asp Trp Met Cys>
____a____a____a____a____a____a____a____a____ORF RF[3] ____a____a____a____a____a____a____>

220 230 240 250 260
* * * * *
CGT TTA CGC CAA CCT GCC TTT GGG ATC AGT TTT GTT CTC TGT ATC TCC TGC ATC
GCA AAT GCG GTT GGA CGG AAA CCC TAG TCA AAA CAA GAG ACA TAG AGG ACG TAG
Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile Ser Cys Ile>
____a____a____a____a____a____a____a____a____ORF RF[3] ____a____a____a____a____a____a____>

270 280 290 300 310 320
* * * * * *
CTT GTG AAA ACT AAT AGA GTA CTC TTA GTA TTT GAA GCC AAG ATC CCC ACA AGT
GAA CAC TTT TGA TTA TCT CAT GAG AAT CAT AAA CTT CGG TTC TAG GGG TGT TCA
Leu Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu Ala Lys Ile Pro Thr Ser>
____a____a____a____a____a____a____a____a____ORF RF[3] ____a____a____a____a____a____a____>

330 340 350 360 370
* * * * *
CTC CAT CGT AAA TGG TGG GGG TTA AAC CTT CAG TTT TTG CTG GTG TTT CTG TGC
GAG GTA GCA TTT ACC ACC CCC AAT TTG GAA GTC AAA AAC GAC CAC AAA GAC ACG
Leu His Arg Lys Trp Trp Gly Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys>
____a____a____a____a____a____a____a____a____a____ORF RF[3] ____a____a____a____a____a____a____>

380 390 400 410 420 430
* * * * * *
ACA TTT GTC CAA GTC ATG ATC TGT GTT GTC TGG CTG TAC AAT GCC CCT CCC TCC
TGT AAA CAG GTT CAG TAC TAG ACA CAA CAG ACC GAC ATG TTA CGG GGA GGG AGG
Thr Phe Val Gln Val Met Ile Cys Val Val Trp Leu Tyr Asn Ala Pro Pro Ser>
____a____a____a____a____a____a____a____a____a____ORF RF[3] ____a____a____a____a____a____a____>

440 450 460 470
* * * * *
AGT TAC AGG AAT TAT GAC ATA GAT GAG ATG ATT TTT ATC ACA TG
TCA ATG TCC TTA ATA CTG TAT CTA CTC TAC TAA AAA TAG TGT AC
Ser Tyr Arg Asn Tyr Asp Ile Asp Glu Met Ile Phe Ile Thr>
____a____a____a____a____a____a____a____a____a____a____a____a____ORF RF[3] ____a____a____a____a____a____>

a cgc cca ggg att gaa aaa ttt gag aag gag atg gag gag cga gac atc 49
Arg Pro Gly Ile Glu Lys Phe Glu Lys Glu Met Glu Glu Arg Asp Ile
1 5 10 15

tgc att cac ctt aat gaa ctt atc tct cag tat ttt gag gay cat gaa 97
Cys Ile His Leu Asn Glu Leu Ile Ser Gln Tyr Phe Glu Asp His Glu
20 25 30

atc caa gcg ctg gct gac agg att gag aac tcc aca gct aaa gtc atc 145
Ile Gln Ala Leu Ala Asp Arg Ile Glu Asn Ser Thr Ala Lys Val Ile
35 40 45

gta gtg ttt gcc agc ggc cca gat atc gag cct tta atc aaa gag atg 193
Val Val Phe Ala Ser Gly Pro Asp Ile Glu Pro Leu Ile Lys Glu Met
50 55 60

gtg agg aga aac atc aca gac cgt atc tgg tta gcc agt gaa gcg tgg 241
Val Arg Arg Asn Ile Thr Asp Arg Ile Trp Leu Ala Ser Glu Ala Trp
65 70 75 80

gct agc tcc tct ctt ata gct aaa cca gag tat ctt gat gtt gtg gct 289
Ala Ser Ser Ser Leu Ile Ala Lys Pro Glu Tyr Leu Asp Val Val Ala
85 90 95

ggg act atc ggc ttt gct ctc aag gca ggg cat att cct ggc tta aga 337
Gly Thr Ile Gly Phe Ala Leu Lys Ala Gly His Ile Pro Gly Leu Arg
100 105 110

gag ttc cta cag caa gtg caa cca aag aga gac agt cat aat gaa ttt 385
Glu Phe Leu Gln Gln Val Gln Pro Lys Arg Asp Ser His Asn Glu Phe
115 120 125

gtc agg gag ttt tgg gaa gaa acc ttc aac tgt tat ctg gaa gac agc 433
Val Arg Glu Phe Trp Glu Glu Thr Phe Asn Cys Tyr Leu Glu Asp Ser
130 135 140

cag aga cag cag gaa agt gag aat ggc agc aca agt ttc agg cct ttg 481
Gln Arg Gln Gln Glu Ser Glu Asn Gly Ser Thr Ser Phe Arg Pro Leu
145 150 155 160

tgt act ggt gag gaa gac atc aca agt gtt gag acc ccg tac ttg gac 529
Cys Thr Gly Glu Asp Ile Thr Ser Val Glu Thr Pro Tyr Leu Asp
165 170 175

tac aca cac ttt cgt atc tcc tat aac gtg tat gtt gca gtt tat tcc 577
Tyr Thr His Phe Arg Ile Ser Tyr Asn Val Tyr Val Ala Val Tyr Ser
180 185 190

att gca cag gcc ctg cag gac ata ctc acc tgc aca cct gga cat gga 625
Ile Ala Gln Ala Leu Gln Asp Ile Leu Thr Cys Thr Pro Gly His Gly
195 200 205

ctc ttt gcc aac aat tcc tgt gcc gat ata aag aaa atg gaa gca tgg 673
Leu Phe Ala Asn Asn Ser Cys Ala Asp Ile Lys Lys Met Glu Ala Trp
210 215 220

100% Encoded Sequence

cag gcc ctg aag cag ctt-aga cat ttg aac tac acc aac agc atg ggg Gln Ala Leu Lys Gln Leu Arg His Leu Asn Tyr Thr Asn Ser Met Gly 225 230 235 240	721
gaa aag atg cac ttt gat gag aac tca gac atg gca tca aac tac acc Glu Lys Met His Phe Asp Glu Asn Ser Asp Met Ala Ser Asn Tyr Thr 245 250 255	769
att ata aac tgg cac cgg tct gct gag gat ggc tct gtg gtg ttt gag Ile Ile Asn Trp His Arg Ser Ala Glu Asp Gly Ser Val Val Phe Glu 260 265 270	817
gac gtg gga tac tac agc atg cac gtc aag aga gga gcc aaa ctg ttc Asp Val Gly Tyr Tyr Ser Met His Val Lys Arg Gly Ala Lys Leu Phe 275 280 285	865
att gac aag aca aag att ttg tgg aat gga tac agt tcg gag gcg cca Ile Asp Lys Thr Lys Ile Leu Trp Asn Gly Tyr Ser Ser Glu Ala Pro 290 295 300	913
ttc tct aat tgc agt gag gac tgt gaa cct ggt aca agg aag ggg atc Phe Ser Asn Cys Ser Glu Asp Cys Glu Pro Gly Thr Arg Lys Gly Ile 305 310 315 320	961
att gac agt atg ccc aca tgt tgc ttt gaa tgc act gag tgc tca gat Ile Asp Ser Met Pro Thr Cys Cys Phe Glu Cys Thr Glu Cys Ser Asp 325 330 335	1009
gga gag tac agt aat cat aaa gat gcc agt gtt tgc acc aag tgt cca Gly Glu Tyr Ser Asn His Lys Asp Ala Ser Val Cys Thr Lys Cys Pro 340 345 350	1057
tat aac tct tgg tcc aat ggg aat cac aca ttc tgc ttc ctg aag gaa Tyr Asn Ser Trp Ser Asn Gly Asn His Thr Phe Cys Phe Leu Lys Glu 355 360 365	1105
atc gag ttt ctc tcc tgg aca gaa cca ttc ggg ata gct ttg gcc ata Ile Glu Phe Leu Ser Trp Thr Glu Pro Phe Gly Ile Ala Leu Ala Ile 370 375 380	1153
tgt gca gta ctg ggt gtg ctc ttg aca gct ttt gtg atc gga gtc ttt Cys Ala Val Leu Gly Val Leu Leu Thr Ala Phe Val Ile Gly Val Phe 385 390 395 400	1201
gtc aga ttc cgc aac acc cca ata gtg aag gcc aca aac cga gaa ctg Val Arg Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn Arg Glu Leu 405 410 415	1249
tcc tac gtt ctc ctg twc tca ctt atc tgt tgc ttc tca agc tcc ctc Ser Tyr Val Leu Leu Xaa Ser Leu Ile Cys Cys Phe Ser Ser Ser Leu 420 425 430	1297
akc ttc atc gg Xaa Phe Ile 435	1308

Arg Pro Gly Ile Glu Lys Phe Glu Lys Glu Met Glu Glu Arg Asp Ile
1 5 10 15
Cys Ile His Leu Asn Glu Leu Ile Ser Gln Tyr Phe Glu Asp His Glu
20 25 30
Ile Gln Ala Leu Ala Asp Arg Ile Glu Asn Ser Thr Ala Lys Val Ile
35 40 45
Val Val Phe Ala Ser Gly Pro Asp Ile Glu Pro Leu Ile Lys Glu Met
50 55 60
Val Arg Arg Asn Ile Thr Asp Arg Ile Trp Leu Ala Ser Glu Ala Trp
65 70 75 80
Ala Ser Ser Ser Leu Ile Ala Lys Pro Glu Tyr Leu Asp Val Val Ala
85 90 95
Gly Thr Ile Gly Phe Ala Leu Lys Ala Gly His Ile Pro Gly Leu Arg
100 105 110
Glu Phe Leu Gln Gln Val Gln Pro Lys Arg Asp Ser His Asn Glu Phe
115 120 125
Val Arg Glu Phe Trp Glu Glu Thr Phe Asn Cys Tyr Leu Glu Asp Ser
130 135 140
Gln Arg Gln Gln Glu Ser Glu Asn Gly Ser Thr Ser Phe Arg Pro Leu
145 150 155 160
Cys Thr Gly Glu Glu Asp Ile Thr Ser Val Glu Thr Pro Tyr Leu Asp
165 170 175
Tyr Thr His Phe Arg Ile Ser Tyr Asn Val Tyr Val Ala Val Tyr Ser
180 185 190
Ile Ala Gln Ala Leu Gln Asp Ile Leu Thr Cys Thr Pro Gly His Gly
195 200 205
Leu Phe Ala Asn Asn Ser Cys Ala Asp Ile Lys Lys Met Glu Ala Trp
210 215 220
Gln Ala Leu Lys Gln Leu Arg His Leu Asn Tyr Thr Asn Ser Met Gly
225 230 235 240
Glu Lys Met His Phe Asp Glu Asn Ser Asp Met Ala Ser Asn Tyr Thr
245 250 255
Ile Ile Asn Trp His Arg Ser Ala Glu Asp Gly Ser Val Val Phe Glu
260 265 270
Asp Val Gly Tyr Tyr Ser Met His Val Lys Arg Gly Ala Lys Leu Phe
275 280 285
Ile Asp Lys Thr Lys Ile Leu Trp Asn Gly Tyr Ser Ser Glu Ala Pro
290 295 300
Phe Ser Asn Cys Ser Glu Asp Cys Glu Pro Gly Thr Arg Lys Gly Ile
305 310 315 320
Ile Asp Ser Met Pro Thr Cys Cys Phe Glu Cys Thr Glu Cys Ser Asp
325 330 335
Gly Glu Tyr Ser Asn His Lys Asp Ala Ser Val Cys Thr Lys Cys Pro
340 345 350
Tyr Asn Ser Trp Ser Asn Gly Asn His Thr Phe Cys Phe Leu Lys Glu
355 360 365
Ile Glu Phe Leu Ser Trp Thr Glu Pro Phe Gly Ile Ala Leu Ala Ile
370 375 380
Cys Ala Val Leu Gly Val Leu Leu Thr Ala Phe Val Ile Gly Val Phe
385 390 395 400
Val Arg Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn Arg Glu Leu
405 410 415
Ser Tyr Val Leu Leu Xaa Ser Leu Ile Cys Cys Phe Ser Ser Ser Leu
420 425 430
Xaa Phe Ile
435

10 20 30 40 50
* * * * *
A CGC CCA GGG ATT GAA AAA TTT GAG AAG GAG ATG GAG GAG CGA GAC ATC TGC
T GCG GGT CCC TAA CTT TTT AAA CTC TTC CTC TAC CTC CTC GCT CTG TAG ACG
Arg Pro Gly Ile Glu Lys Phe Glu Lys Glu Met Glu Glu Arg Asp Ile Cys>
____a____a____a____a____a____a____ORF RF[2] ____a____a____a____a____a____a____>

60 70 80 90 100
* * * * *
ATT CAC CTT AAT GAA CTT ATC TCT CAG TAT TTT GAG GAY CAT GAA ATC CAA GCG
TAA GTG GAA TTA CTT GAA TAG AGA GTC ATA AAA CTC CTR GTC CTT TAG GTT CGC
Ile His Leu Asn Glu Leu Ile Ser Gln Tyr Phe Glu Asp His Glu Ile Gln Ala>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

110 120 130 140 150 160
* * * * * *
CTG GCT GAC AGG ATT GAG AAC TCC ACA GCT AAA GTC ATC GTA GTG TTT GCC AGC
GAC CGA CTG TCC TAA CTC TTG AGG TGT CGA TTT CAG TAG CAT CAC AAA CGG TCG
Leu Ala Asp Arg Ile Glu Asn Ser Thr Ala Lys Val Ile Val Val Phe Ala Ser>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

170 180 190 200 210
* * * * *
GGC CCA GAT ATC GAG CCT TTA ATC AAA GAG ATG GTG AGG AGA AAC ATC ACA GAC
CCG GGT CTA TAG CTC GGA AAT TAG TTT CTC TAC CAC TCC TCT TTG TAG TGT CTG
Gly Pro Asp Ile Glu Pro Leu Ile Lys Glu Met Val Arg Arg Asn Ile Thr Asp>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

220 230 240 250 260
* * * * *
CGT ATC TGG TTA GCC AGT GAA GCG TGG GCT AGC TCC TCT CTT ATA GCT AAA CCA
GCA TAG ACC AAT CGG TCA CTT CGC ACC CGA TCG AGG AGA GAA TAT CGA TTT GGT
Arg Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Leu Ile Ala Lys Pro>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

270 280 290 300 310 320
* * * * * *
GAG TAT CTT GAT GTT GTG GCT GGG ACT ATC GGC TTT GCT CTC AAG GCA GGG CAT
CTC ATA GAA CTA CAA CAC CGA CCC TGA TAG CCG AAA CGA GAG TTC CGT CCC GTA
Glu Tyr Leu Asp Val Val Ala Gly Thr Ile Gly Phe Ala Leu Lys Ala Gly His>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

330 340 350 360 370
* * * * *
ATT CCT GGC TTA AGA GAG TTC CTA CAG CAA GTG CAA CCA AAG AGA GAC AGT CAT
TAA GGA CCG AAT TCT CTC AAG GAT GTC GTT CAC GTT GGT TTC TCT CTG TCA GTA
Ile Pro Gly Leu Arg Glu Phe Leu Gln Gln Val Gln Pro Lys Arg Asp Ser His>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

380 390 400 410 420 430
* * * * * *
AAT GAA TTT GTC AGG GAG TTT TGG GAA GAA ACC TTC AAC TGT TAT CTG GAA GAC
TTA CTT AAA CAG TCC CTC AAA ACC CTT CTT TGG AAG TTG ACA ATA GAC CTT CTG
Asn Glu Phe Val Arg Glu Phe Trp Glu Glu Thr Phe Asn Cys Tyr Leu Glu Asp>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

440 450 460 470 480
* * * * *
AGC CAG AGA CAG CAG GAA AGT GAG AAT GGC AGC ACA AGT TTC AGG CCT TTG TGT
TCG GTC TCT GTC GTC CTT TCA CTC TTA CCG TCG TGT TCA AAG TCC GGA AAC ACA
Ser Gln Arg Gln Gln Glu Ser Glu Asn Gly Ser Thr Ser Phe Arg Pro Leu Cys>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

490 500 510 520 530
* * * * *
ACT GGT GAG GAA GAC ATC ACA AGT GTT GAG ACC CCG TAC TTG GAC TAC ACA CAC
TGA CCA CTC CTT CTG TAG TGT TCA CAA CTC TGG GGC ATG AAC CTG ATG TGT GTG
Thr Gly Glu Glu Asp Ile Thr Ser Val Glu Thr Pro Tyr Leu Asp Tyr Thr His>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

540 550 560 570 580 590
* * * * * *
TTT CGT ATC TCC TAT AAC GTG TAT GTT GCA GTT TAT TCC ATT GCA CAG GCC CTG
AAA GCA TAG AGG ATA TTG CAC ATA CAA CGT CAA ATA AGG TAA CGT GTC CGG GAC
Phe Arg Ile Ser Tyr Asn Val Tyr Val Ala Val Tyr Ser Ile Ala Gln Ala Leu>
____d____a____a____a____o____a____a____a____a____a____a____a____a____a____a____>

600 610 620 630 640
* * * * *
CAG GAC ATA CTC ACC TGC ACA CCT GGA CAT GGA CTC TTT GCC AAC AAT TCC TGT
GTC CTG TAT GAG TGG ACG TGT GGA CCT GTA CCT GAG AAA CGG TTG TTA AGG ACA
Gln Asp Ile Leu Thr Cys Thr Pro Gly His Gly Leu Phe Ala Asn Asn Ser Cys>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

650 660 670 680 690 700
* * * * * *
GCC GAT ATA AAG AAA ATG GAA GCA TGG CAG GCC CTG AAG CAG CTT AGA CAT TTG
CGG CTA TAT TTC TTT TAC CTT CGT ACC GTC CGG GAC TTC GTC GAA TCT GTA AAC
Ala Asp Ile Lys Lys Met Glu Ala Trp Gln Ala Leu Lys Gln Leu Arg His Leu>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

710 720 730 740 750
* * * * *
AAC TAC ACC AAC AGC ATG GGG GAA AAG ATG CAC TTT GAT GAG AAC TCA GAC ATG
TTG ATG TGG TTG TCG TAC CCC CTT TTC TAC GTG AAA CTA CTC TTG AGT CTG TAC
Asn Tyr Thr Asn Ser Met Gly Glu Lys Met His Phe Asp Glu Asn Ser Asp Met>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

760 770 780 790 800
* * * * *
GCA TCA AAC TAC ACC ATT ATA AAC TGG CAC CGG TCT GCT GAG GAT GGC TCT GTG
CGT AGT TTG ATG TGG TAA TAT TTG ACC GTG GCC AGA CGA CTC CTA CGG AGA CAC
Ala Ser Asn Tyr Thr Ile Ile Asn Trp His Arg Ser Ala Glu Asp Gly Ser Val>
____g____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

810 820 830 840 850 860
* * * * * *
GTG TTT GAG GAC GTG GGA TAC TAC AGC ATG CAC GTC AAG AGA GGA GGC AAA CTG
CAC AAA CTC CTG CAC CCT ATG ATG TCG TAC GTG CAG TTC TCT CCT CGG TTT GAC
Val Phe Glu Asp Val Gly Tyr Tyr Ser Met His Val Lys Arg Gly Ala Lys Leu>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

870 880 890 900 910
* * * * *
TTC ATT GAC AAG ACA AAG ATT TTG TGG AAT GGA TAC AGT TCG GAG GCG CCA TTC
AAG TAA CTG TTC TGT TTC TAA AAC ACC TTA CCT ATG TCA AGC CTC CGC GGT AAG
Phe Ile Asp Lys Thr Lys Ile Leu Trp Asn Gly Tyr Ser Ser Glu Ala Pro Phe>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

920 930 940 950 960 970
* * * * * *
TCT AAT TGC AGT GAG GAC TGT GAA CCT GGT ACA AGG AAG GGG ATC ATT GAC AGT
AGA TTA ACG TCA CTC CTG ACA CTT GGA CCA TGT TCC TTC CCC TAG TAA CTG TCA
Ser Asn Cys Ser Glu Asp Cys Glu Pro Gly Thr Arg Lys Gly Ile Ile Asp Ser>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

980 990 1000 1010 1020

* * * * *

ATG CCC ACA TGT TGC TTT GAA TGC ACT GAG TGC TCA GAT GGA GAG TAC AGT AAT
TAC GGG TGT ACA ACG AAA CTT ACG TGA CTC ACG AGT CTA CCT CTC ATG TCA TTA
Met Pro Thr Cys Cys Phe Glu Cys Thr Glu Cys Ser Asp Gly Glu Tyr Ser Asn>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

1030 1040 1050 1060 1070

* * * * *

CAT AAA GAT GCC AGT GTT TGC ACC AAG TGT CCA TAT AAC TCT TGG TCC AAT GGG
GTA TTT CTA CGG TCA CAA ACG TGG TTC ACA GGT ATA TTG AGA ACC AGG TTA CCC
His Lys Asp Ala Ser Val Cys Thr Lys Cys Pro Tyr Asn Ser Trp Ser Asn Gly>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

1080 1090 1100 1110 1120 1130

* * * * * *

AAT CAC ACA TTC TGC TTC CTG AAG GAA ATC GAG TTT CTC TCC TGG ACA GAA CCA
TTA GTG TGT AAG ACG AAG GAC TTC CTT TAG CTC AAA GAG AGG ACC TGT CTT GGT
Asn His Thr Phe Cys Phe Leu Lys Glu Ile Glu Phe Leu Ser Trp Thr Glu Pro>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

1140 1150 1160 1170 1180

* * * * *

TTC GGG ATA GCT TTG GCC ATA TGT GCA GTA CTG GGT GTG CTC TTG ACA GCT TTT
AAG CCC TAT CGA AAC CGG TAT ACA CGT CAT GAC CCA CAC GAG AAC TGT CGA AAA
Phe Gly Ile Ala Leu Ala Ile Cys Ala Val Leu Gly Val Leu Leu Thr Ala Phe>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

1190 1200 1210 1220 1230 1240

* * * * * *

GTG ATC GGA GTC TTT GTC AGA TTC CGC AAC ACC CCA ATA GTG AAG GCC ACA AAC
CAC TAG CCT CAG AAA CAG TCT AAG GCG TTG TGG GGT TAT CAC TTC CGG TGT TTG
Val Ile Gly Val Phe Val Arg Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

1250 1260 1270 1280 1290

* * * * *

CGA GAA CTG TCC TAC GTT CTC CTG TWC TCA CTT ATC TGT TGC TTC TCA AGC TCC
GCT CTT GAC AGG ATG CAA GAG GAC AWG AGT GAA TAG ACA ACG AAG AGT TCG AGG
Arg Glu Leu Ser Tyr Val Leu Leu Xxx Ser Leu Ile Cys Cys Phe Ser Ser Ser>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

1300

*

CTC AKC TTC ATC GG
GAG TMG AAG TAG CC
Leu Xxx Phe Ile>
____a____a____a____a____a____a____a____a____a____a____a____a____a____a____>

Docket No.: 2856.1001-011
Title: "Polycation-Sensing Receptor ..."
Inventors: H. William Harris, *et al.*

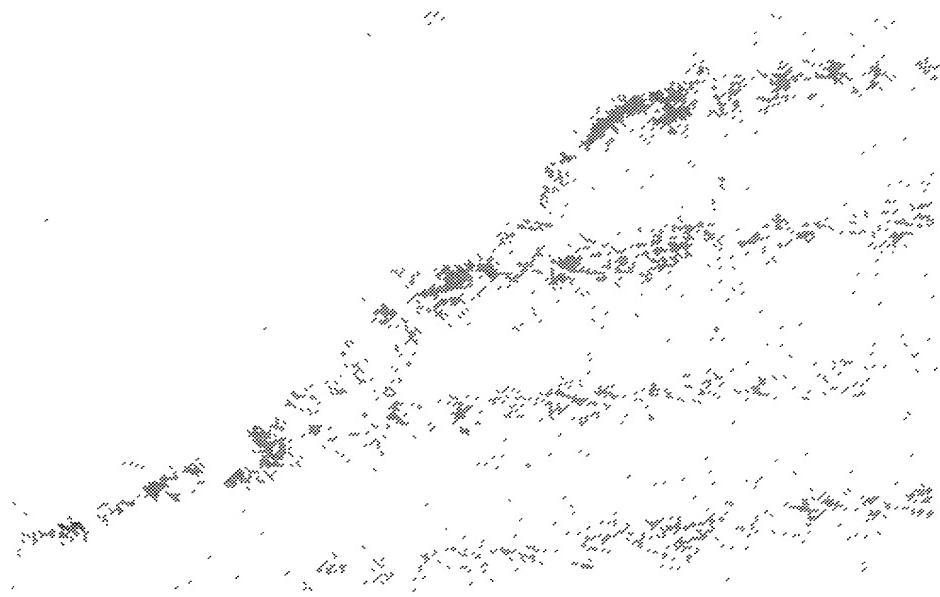


FIG. 31A

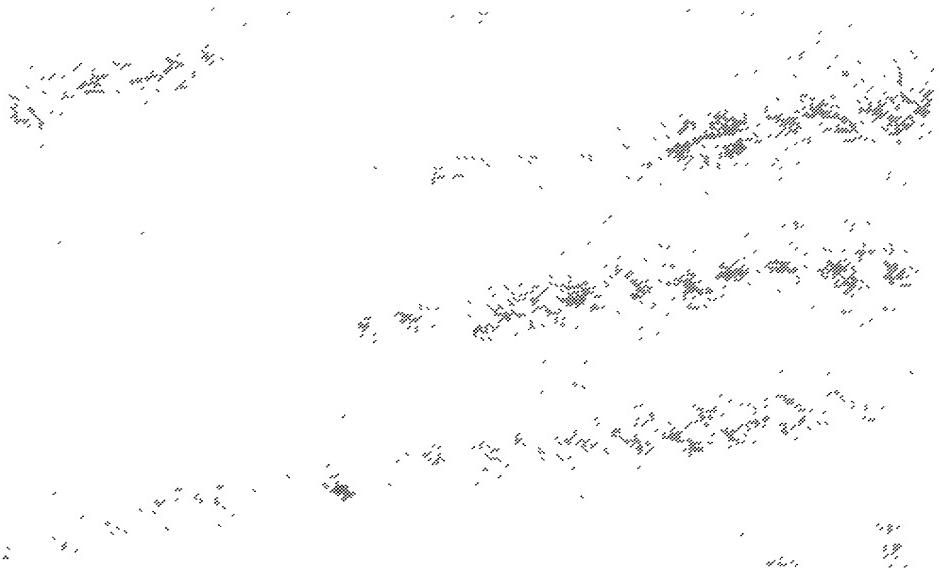


FIG. 31B